

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2001, 09:41:15 ; Search time 94.04 Seconds

(without alignments)  
2168.100 Million cell updates/sec

Title: US-09-006-352-1

Perfect score: 1077

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Scoring table:  
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Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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5: /cgn2\_6/ptodata/2/lna/PCrUS.COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	103	9.6	1355	3	US-08-974-022-5
6	76	7.1	3331	4	US-09-042-785A-1
7	68	6.3	759	4	US-09-042-785A-6
8	68	6.3	1815	4	US-09-042-785A-24
9	68	6.3	2186	3	US-08-959-382-1
10	68	6.3	2612	4	US-09-042-785A-3
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13	54.8	5.1	1164	2	US-08-794-796-1
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15	53.8	5.0	1641	1	US-08-385-229-1
16	53.8	5.0	1641	2	US-08-650-000-1
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18	53.8	5.0	2224	4	US-08-477-347-2
19	52.2	4.8	1931	3	US-09-019-942-2
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21	52	4.8	2793	1	US-08-458-298-1
22	51.6	4.8	3796	2	US-08-762-308-11
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24	51.6	4.8	3813	6	5395760-3
25	49.6	4.6	691	1	US-08-266-080B-12
26	49.6	4.6	691	5	PCR-US95-05423-12
27	49.4	4.6	8906	2	US-08-826-267-1

28	48.6	4.5	1878	3	US-08-996-139-14	Sequence 14, Appl
29	48.6	4.5	1878	4	US-08-995-659-14	Sequence 14, Appl
30	47.8	4.4	3581	2	US-08-738-349-1	Sequence 1, Appl
31	47.2	4.4	1057	1	US-08-147-784-1	Sequence 1, Appl
32	47.2	4.4	1057	1	US-08-195-967-1	Sequence 1, Appl
33	47	4.4	397	3	US-09-253-691-3	Sequence 3, Appl
34	46.6	4.3	543	6	5273901-6	Patent No. 5273901
35	46.6	4.3	1505	2	US-08-909-965C-13	Sequence 13, Appl
36	45.6	4.2	547	1	US-08-131-365B-41	Sequence 41, Appl
37	45.6	4.2	547	2	US-08-668-123-41	Sequence 41, Appl
38	45.4	4.2	1578	4	US-09-044-404A-1	Sequence 1, Appl
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41	45.2	4.2	2635	3	US-09-126-280-3	Sequence 3, Appl
42	45.2	4.2	2670	3	US-09-126-280-1	Sequence 1, Appl
43	45.2	4.2	2961	2	US-08-407-875-1	Sequence 1, Appl
44	45	4.2	848	1	US-08-192-480A-1	Sequence 1, Appl
45	45	4.2	1582	3	US-08-545-196B-10	Sequence 10, Appl

#### ALIGNMENTS

RESULT 1  
US-08-794-796-1  
; Sequence 1, Application US/08794796  
; Patent No. 5885800  
; GENERAL INFORMATION:  
; APPLICANT: Emery, John  
; APPLICANT: Tan, KB  
; APPLICANT: Truneh, Alem  
; APPLICANT: Young, Peter  
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
; TITLE OF INVENTION: TR4  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: PastSeq for Windows Version 2.0  
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; APPLICATION NUMBER: US/08/794,796  
; FILING DATE: 04-FEB-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Han, William T  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: GH50000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-4026  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1164 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
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OY 301 gctcctgag 360  
Db 387 gctccttgcgag 446  
OY 361 tgcctggttgcgctgctgctgctgctgctgctgctgctgctgctgctgctg 420  
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OY 481 tgcctggttgcgctgctgctgctgctgctgctgctgctgctgctgctgctg 540  
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; Sequence 47; Application us/08997918  
; Patent No. 6077689  
; GENERAL INFORMATION:  
; APPLICANT: Snavely, Marshall D.  
; TITLE OF INVENTION: ENHANCED SOLUBILITY OF RECOMBINANT PROTEINS  
; FILE REFERENCE: A-496  
; CURRENT APPLICATION NUMBER: US/08/997,918  
; CURRENT FILING DATE: 1997-12-24  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: Patentlin Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 525  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
US-08-997-918-47

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Best Local Similarity 53.6%; Pred. No. 4.9e-18;  
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OY 302 tccctctgcgag 361  
Db 194 cgglttgcag 253  
OY 362 gccgctgcgag 421  
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OY 422 cactgtgctgcgag 481  
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OY 482 gcccccag 541  
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OY 542 acgag 601  
Db 434 acgag 601  
OY 602 gcacccag 625  
Db 494 gctcggtaactcggagtgagacc 517

RESULT 3  
US-08-974-022-1  
; Sequence 1; Application us/08974022  
; Patent No. 6015938  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.



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3      Sequence 5, Application US/08974022
4      Patent No. 6015938
5      GENERAL INFORMATION:
6      APPLICANT: Boyle, William J.
7      APPLICANT: Lacey, David L.
8      APPLICANT: Calzone, Frank J.
9      APPLICANT: Chang, Ming-Shi
10     TITLE OF INVENTION: OSTEOPROTEGERIN
11     NUMBER OF SEQUENCES: 53
12     CORRESPONDENCE ADDRESS:
13     ADDRESSEE: Amgen Inc.
14     STREET: 1840 Dehavenland Drive
15     CITY: Thousand Oaks
16     STATE: California
17     COUNTRY: USA
18     ZIP: 91320-1789
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: PatentIn Release #1.0, Version #1.30
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/08/974,022
26     FILING DATE: 12-DEC-1995
27     CLASSIFICATION:
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: 08/577,788
30     FILING DATE:
31     ATTORNEY/AGENT INFORMATION:
32     NAME: Winter, Robert B.
33     REFERENCE/DOCKET NUMBER: A-378
34     INFORMATION FOR SEQ ID NO: 5:
35     SEQUENCE CHARACTERISTICS:
36     LENGTH: 1355 base pairs
37     TYPE: nucleic acid
38     STRANDEDNESS: single
39     TOPOLOGY: linear
40     MOLECULE TYPE: cDNA
41     FEATURE:
42     NAME/KEY: CDS
43     LOCATION: 94..1296
44     US-08-974-022-5

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3      Sequence 1, Application US/09042785A
4      Patent No. 6194151
5      GENERAL INFORMATION:
6      APPLICANT: Busfield, Samantha J
7      TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
8      NUMBER OF SEQUENCES: 31
9      CORRESPONDENCE ADDRESS:
10     ADDRESSEE: LAHIVE & COCKFIELD, LLP
11     STREET: 28 State Street
12     CITY: Boston
13     STATE: Massachusetts
14     COUNTRY: USA
15     ZIP: 02109
16     COMPUTER READABLE FORM:
17     MEDIUM TYPE: Floppy disk
18     COMPUTER: IBM PC compatible
19     OPERATING SYSTEM: PC-DOS/MS-DOS
20     SOFTWARE: Patent Release #1.0, Version #1.25
21     CURRENT APPLICATION DATA:
22     APPLICATION NUMBER: US/09/042,785A
23     FILING DATE: 17-MAR-1998
24     PRIOR APPLICATION DATA:
25     APPLICATION NUMBER: US 08/938,896
26     FILING DATE: 26-SEP-1997
27     ATTORNEY/AGENT INFORMATION:
28     NAME: Mandragouras, Amy E
29     REGISTRATION NUMBER: 36,207
30     REFERENCE/DOCKET NUMBER: MEI-001CP
31     TELECOMMUNICATION INFORMATION:
32     TELEPHONE: (617)742-4214
33     INFORMATION FOR SEQ ID NO: 1:
34     SEQUENCE CHARACTERISTICS:
35     LENGTH: 331 base pairs
36     TYPE: nucleic acid
37     STRANDEDNESS: single
38     TOPOLOGY: linear
39     MOLECULE TYPE: CDNA
40     FEATURE:
41     NAME/KEY: CDS
42     LOCATION: 344..2065
43     US-09-042-785A-1

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GenCore version 4.5  
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Run on: November 2, 2001, 13:30:49 ; Search time 39.52 Seconds  
(without alignments)  
3880.112 Million cell updates/sec

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Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*  
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6: /cgn2\_6/ptodata/2/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	810	100.0	1164	2	US-08-794-796-1
2	129.6	16.0	525	3	US-08-997-918-47
3	112	13.8	2432	3	US-08-974-022-1
4	110.4	13.6	1324	3	US-08-974-022-3
5	103	12.7	1355	3	US-08-974-022-5
6	76	9.4	3331	4	US-09-042-785A-1
7	68	8.4	759	4	US-09-042-785A-6
8	68	8.4	1815	4	US-09-042-785A-24
9	68	8.4	2186	3	US-08-959-382-1
10	68	8.4	2612	4	US-09-042-785A-3
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14	52	6.4	2793	1	US-08-209-747-1
15	52	6.4	2793	1	US-08-458-298-1
16	51.6	6.4	3796	2	US-08-762-308-11
17	51.6	6.4	3813	2	US-08-650-000-3
18	51.6	6.4	3813	6	5395760-3
19	49.6	6.1	691	1	US-08-266-0808-12
20	49.6	6.1	691	1	PC1-US95-05423-12
21	49.4	6.0	8906	2	US-08-826-267-1
22	48.6	6.0	1878	3	US-08-996-139-14
23	48.6	6.0	1878	4	US-08-995-659-14
24	48	5.9	1557	1	US-08-385-229-3
25	48	5.9	1641	1	US-08-385-229-1
26	48	5.9	1641	2	US-08-650-000-1
27	48	5.9	1641	6	5395760-1

28	48	5.9	2224	4	US-08-477-347-2	Sequence 2, Appl
29	47	5.8	397	3	US-09-253-691-3	Sequence 3, Appl
30	46.6	5.8	543	6	5273901-6	Patent No. 5273901
31	45.4	5.6	1057	4	US-08-147-784-1	Sequence 1, Appl
32	45.4	5.6	1057	4	US-08-195-967-1	Sequence 1, Appl
33	45.2	5.6	203	4	US-09-043-303-7	Sequence 7, Appl
34	45.2	5.6	2635	3	US-09-126-280-3	Sequence 3, Appl
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#### ALIGNMENTS

RESULT 1  
US-08-794-796-1  
Sequence 1, Application US/08794796  
Patent No. 5885800  
GENERAL INFORMATION:  
APPLICANT: Emery, John  
APPLICANT: Tan, KB  
APPLICANT: Truneh, Alem  
APPLICANT: Young, Peter  
TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794, 796  
FILING DATE: 04-FEB-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Han, William T  
REGISTRATION NUMBER: 34,344  
REFERENCE/DOCKET NUMBER: GH50000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5219  
TELEFAX: 610-270-4026  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1164 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-794-796-1  
Query Match 100.0%; Score 810; DB 2; Length 1164;

Best Local Similarity 100.0%; Pred. No. 5.6e-150;  
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	gcaaaacacccaccattaccccttgcgcggagacgcagaaagacagagagagcgcgtgcatgtgcgc	60
Dp	201	GCAGAAACACCCACTTACCCCTGGCGGAGACCGAAGACAGGGAGCGGCTGctgtgtggcc	260
QY	61	caatgccccccagagcaaccttgtgtcagcgcgtgtgcgcgcgagacagcccaacgaagt	120
Dp	261	CAGTgccccccAGGACACCTTGTGTCAAGGCGCGGCGCGGAGACACCCACGACCTGT	320
QY	121	ggcccggtgtccacgcgcgcacatacagcaagttctgtgaactacctgtgagcgtcgcgtac	180
Dp	321	GGCCGCTGTCCACGCGCGCATTCACACGATGTGGAATACCTGCGAGCCCTGCGGTAC	380
QY	181	tgcacagctctctctgcgggagcgcgaaagagagagacacgcgcgtgtgcacgcaccccaac	240
Dp	381	TGCACAGCTCCTCTCGGGGAGCGTAGAGAGAGGACACGGCTTGGCCACGCCACCCACAC	440
QY	241	cgttcacctgcgcctgcgcgcacgcgcgtctctgcgcgcgcgtgttctctgtctgtgagcaga	300
Dp	441	CGTCCCTGCGCCTCTCGCACCGGCTTCTTGCGCGCACGCTGTTTCTGTCTGTGAGACGCA	500
QY	301	tcgcttcaacctgtgtgcgcgcgtgtattgcgcgcggagaccccgacgcagaaacacgcagtcg	360
Dp	501	TCTGTCTCACCTGTGATGCCGCGGTATTTGCCCGCGGCACCCGACCCGACGAAACCCGACTGC	560
QY	361	caagcgcgtgccccccagaggaaccttctaaagcagcagcttcacgcttcagagcagtgccagccc	420
Dp	561	CAGCCGTGCCCCCGAGGACCTTGTCAAGCAGCAGCTTCACGCTCAGGCTCAGGCTCAGGCC	620
QY	421	caaccgcacatgcacgcgcctgtgagcctgcgcctcaatgtgtcacagcctctctctccatgac	480
Dp	621	CACGCAACTGCACAGGGCCTTGCGCTGACCCTCAATGTGCAGAGCTTCTCTCCCATGAC	680
QY	481	accctgtgcacacagctgtgcactgagcttccccctcagcacacagaggttaccagagacttgagag	540
Dp	681	ACCTGTGCACACACTGCACAGGCTTCCCCCTCAGCACACGAGGTACAGAGAGCTGAGAG	740
QY	541	tgttaagcgtgcgcgtacacgcgaattgtgtgcttctccagacacatctccatccagagagctgca	600
Dp	741	TGTGAGCGTGCGTCATTCGACTTGTGTGCTTCCAGGACATCTTCATCAGAGAGCTGCAG	800
QY	601	cgagctgtgcagagccctcgc	660
Dp	801	CGGCTGTGCAGAGCCCTTCAGAGCCCGCGAGAGGCTGAGGCTCCGACACCCAGAGCGCGGCTC	860
QY	661	ggagccttgtagcgtggaagcgtgcttgcgcgtctcaagagcttctctggggcgcgaagcagag	720
Dp	861	GCGGCTTTCAGAGCTGTGAGAGCTGTGCTGCGGCTTCACGAGCTCTCTGGGGGCGCAGAGCGG	920
QY	721	gcgcctgtgtgtgcgcgtctgtcagcagcgcgtgcgcgtgtgcagagatgccgcgggtctgagcgcg	780
Dp	921	GCGGTGTGTGTGCGGCTGTGCTCAGAGCCCTTCGCGGTGCGCAGGATGCCCGGCGGTGAGCGG	980
QY	781	agcgttcgtagcgccttccctccctgtgtgac	810
Dp	981	AGCCTCGTAGCGCTTCTCTCCGTGTGAC	1010

RESULT 2  
 US-08-997-918-47  
 Sequence 47, Application US/08997918  
 Patent No. 6077689  
 GENERAL INFORMATION:  
 APPLICANT: Snaively, Marshall D.  
 TITLE OF INVENTION: ENHANCED SOLUBILITY OF RECOMBINANT PROTEINS  
 FILE REFERENCE: A-496  
 CURRENT APPLICATION NUMBER: US/08/997,918  
 CURRENT FILING DATE: 1997-12-24  
 NUMBER OF SEQ ID NOS: 59  
 SOFTWARE: SeqMan Ver. 2.1  
 SEQ ID NO 47

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; LENGTH:525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: Fragment encoding amino acids 22-194 of human OPO
SI-08-997-918-47

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Query Match	16.0%;	Score 129.6;	DB 3;	Length 525;
Best Local Similarity	53.6%;	Pred. No. 1.7e-17;		
Matches 270; Conservative	0;	Mismatches 234;	Indels 0;	Gaps 0

[illegible]

RESULT 3  
 US-08-974-022-1  
 : Sequence 1 Application US/08974022  
 : Patent No. 6015938  
 : GENERAL INFORMATION:  
 : APPLICANT: Boyle, William J.  
 : APPLICANT: Lacey, David L.  
 : APPLICANT: Calzone, Frank J.  
 : APPLICANT: Chang, Ming-Shi  
 : TITLE OF INVENTION: OSTROPROTEGERIN  
 : NUMBER OF SEQUENCES: 53  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Amgen Inc.  
 : STREET: 1840 Dehavenland Drive  
 : City: Thousand Oaks  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 91320-1789  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1326
US-08-974-022-1

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```

Query Match      13.8%; Score 112; DB 3; Length 2432;
Best Local Similarity 52.3%; Pred. No. 5.1e-14;
Matches 247; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

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QY 28 gacgcagagacagggagggcgctgtgtgctgcccagccagcacttgtgag 87
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 217 GACCCAGAAACCGGACGCTCAGCTCTGTGTGACAAATGCTCTCTGACCTACTACTAAA 276
QY 88 cggcgcgtgcccgcagagacagcccaagcagctgtgcccgtgtccacgcgcactacag 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 277 CAGCAGCTGACAGTCAAGAGAGAGACACTGTGTGCTCCCTTGCCCTGACTCTTATACG 336
QY 148 cagttctggaactaactgtgagcgctgcgtactgtcaagctcctctcggggagcgtag 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 337 GACAGCTGCGACACGAGTGAATGATGCTGTACTGACGCCCGCTGTGCAAGAACTGACAG 396
QY 208 gagggagagcgagcgtgtgcccagcccaagacgctgcccgcgtgcagcagcgcttc 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 397 ACCGCTGAAGAGAGTGCACACCCAGCCACACCGAGTGTGCGAATGTGAGAAAGGCGCC 456
QY 268 ttcgcagcagctgtgtctgtgtgagcagcagctcgtgtccactgtgtgcgcgctgagt 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 457 TACCTGGAGCTCAATTCCTCTTGAAGCAGCGAGCTGTCCCGCAGGCTTGGGTGTCTG 516
QY 328 gccccgggacccccagcagacagcagctgcccagcgtgtgccccagcagccttctca 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 517 CAGGCTGGGACCCAGAGCCAAACACGCTTTCGAAAAGATGTCGGATGCGTTCTTCTCA 576
QY 388 gccagcagcctcagctcagagcagctgcccagcccaagcagcagcagcagcagcagctg 447
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 577 GGTGAGACGTTCATCGAAAGACCCCTGTAGGAAACACACCACTGCACTTGTGGCTTC 636
QY 448 gccctcaatgtgcagagctcttcctccatgacacccctgtgcaacagctgca 499
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 637 CTGCTAATTGAGAAAGAAATGCAACATGATGTATGTTCGGGAAACA 688

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RESULT 4
US-08-974-022-3
Sequence 3, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.

```

```

STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1324 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..1292
US-08-974-022-3

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Query Match      13.6%; Score 110.4; DB 3; Length 1324;
Best Local Similarity 52.1%; Pred. No. 9.8e-14;
Matches 246; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

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QY 28 gacgcagagacagggagggcgctgtgtgctgcccagccagcacttgtgag 87
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 183 GACCCAGAAACCGGACGCTCAGCTCTGTGTGACAAATGCTCTCTGACCTACTACTAAA 242
QY 88 cggcgcgtgcccgcagagacagcccaagcagctgtgcccgtgtccacgcgcactacag 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 243 CAGCAGCTGACAGTCAAGAGAGAGACACTGTGTGCTCCCTTGCCCTGACTCTTATACG 302
QY 148 cagttctggaactaactgtgagcgctgcgtactgtcaagctcctctcggggagcgtag 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 303 GACAGCTGCGACACGAGTGAATGATGCTGTACTGACGCCCGCTGTGCAAGAACTGACAG 362
QY 208 gagggagagcgagcgtgtgcccagcccaagacgctgcccgcgtgcagcagcgcttc 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 363 TCCGTAAGAGAGAGTGCACACCCAGCCACACCGAGTGTGTAGTGTGAGAAAGGCGCT 422
QY 268 ttcgcagcagctgtgtctgtgtgagcagcagctcgtgtccactgtgtgcgcgctgagt 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 423 TACCTGGAGCTCAATTCCTCTTGAAGCAGCGAGCTGTCCCGCAGGCTTGGGTGTG 482
QY 328 gccccgggacccccagcagacagcagctgcccagcgtgtgccccagcagccttctca 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 483 CAAGCTGGAACCCAGAGCCAAACACGTTTCGAAAAGATGTCAGATGCGTTCTTCTCA 542
QY 388 gccagcagcctcagctcagagcagctgcccagcccaagcagcagcagcagcagcagctg 447
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 543 GGTGAGACGTTCATCGAAAGACCCCTGTATAAACACAGAACTGCACTTGTGGCTTC 602
QY 448 gccctcaatgtgcagagctcttcctccatgacacccctgtgcaacagctgca 499
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 603 CTGCTAATTGAGAAAGAAATGCAACATGATGTATGTTCGGGAAACA 654

```

```

RESULT 5
US-08-974-022-5
Sequence 5, Application US/08974022

```

Patent No. 6015938  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO.: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1355 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 94..1296  
US-08-974-022-5

Db	527	GTCCAGATGGGTCTTTCACAAATGAGACGTCATCTAAAGCACCCTGTGAAAAACAGACAA	586
Oy	428	atcgacagcccttggccttgcctgaatgctgcagccttcctcccaatgacctgtc	487
Db	587	ATTGACAGTCTCTTTTGGTCTCTCGTAACTCAGAAAGGAATATCAACACACACATAT	646
Oy	488	gcacacagctgcaatg	502
Db	647	GTTCGGGAAACAGTG	661

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RESULT 6
US-09-042-785A-1
Sequence 1, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3331 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 344..2065
US-09-042-785A-1

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[illegible]

	Query Match	Similarity	9.4%	Score	76	DB	4:	Length	3331	
	Best Local Similarity	9.4%	Pred.	No. 5,3e-07						
	Matches	228;	Conservative	0;	Mismatches	270;	Indels	0;	Gaps	0;
OY	12	CACCTACCCTCGGCGAGCAGCAACAAGGGAGCGGTGTGTGTGCACATGCCCCC	71							
Db	253	CACCTACCCGCATGTTTGACCGTACCACGTGGCCAGGTGTGAACCTGCCAACAAAGTGGCCAGC	312							
OY	72	aggacaccttctgtgcagcagcgcgctgcccgcgcgaacaagccccaagaactgttgccccgtgcc	131							
Db	313	AGGAACGTATTGTCCTCGGACCACTTGACCAACATGACCGCTCGGACTCTGCGAGCATGGCCC	372							
OY	132	accgcgcactcaaacgcagattctgaaactactctggtagcgctcgcgtactatgcacagtctt	191							
Db	373	CGCGGGGACCTTTACCCAGGCACGAAGAAGGAGTATGAGATGCCATATCATCTGTGTGTGAGCC	432							

Qy	192	ctgcgagggagcgtgagaggaagaggaagcaggctctgcacagccaccccaacacgcgtccctgcg	251
Db	433	ATGTCACATGCGCCGATGATTTGAGAGATTACCTTTGCTGCGCTTGCCTGACTACCCAGAGTGCAT	422
Qy	252	ctgcgcacacagcgtctctcgcgcacgcctgtgtctctgtctgagagacacatcgtgtccac	311
Db	493	CTGCGCCACNCTGGATGTGATCATGTTATATGTAAGTACTGGCTCCCATACACTGTGTCCCGT	552
Qy	312	tggtgtcgcgctgtatctgcgcccggaaccccccagacagaacacagctgtccagcgcgtgtcc	371
Db	553	GGGCTGGGGGTGTGGCGAAGAAAGGAGCAGAGAAATGAAGATGTGGCTGTGAAGCAGTGCGC	612
Qy	372	cccaaggcacctctctcagccagcagctccagctcagagcagtgccagcccccacccagcaacty	431
Db	613	TGCGGGGTACCTTCTCTCAGACGCGCCCTTCACAGTGTGATACAGTGTAAACCTCACACGAGCTG	672
Qy	432	cacgagcccttgagcctgtgcccctcaatctgtgcaggctctctccctccatgacacacctgtgac	491
Db	673	TCTGGGTAGAACCTGTGAGGGGTCTAAGCAGGGAGCCAGAGAGACAGACAACCTGTGTGG	732
Qy	492	cagctgcacatgctctcccccctgcacac	519
Db	733	CATGCGCCTGTCTTCTTCACACACAAC	760

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RESULT 7
US-09-042-785A-6
Sequence 6, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..759
US-09-042-785A-6

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Query Match	8.48;	Score 68;	DB 4;	Length 759;
Best Local Similarity	45.98;	Pred. No. 1.7e-05;		
Matches: 233;	Conservative	0;	Mismatches 275;	Indels 0;
				Gaps 0;

OY	12	cactcaacccctcgcgagcgagcaagaagggagcagctgltgagcccaatgagccccc	71
Db	156	CACATACCGGCATGTTGACCGGTGCACCGGGCAAGGTCTTAACCTGTATCAAGTGTCCAGC	215
OY	72	agcaacettltgtagcagcgccgtgtccgcgcagacagccccaagcagctgtgcccgttcc	131
Db	216	AGGAACCTATGTCTCTGTAGGCAATTGTACCACACAAGCCTTGCGCCTCTGCACGATTTGCC	275
OY	132	accgcgcacatcacacacgcagtlctltgaaactaactltyagcgtctgcgcctatactgcaacgtcct	191
Db	276	TGTGGGGACCTTTACACAGCATGAGAAATGCGATFAGAGAAATGCCATGACGTGTGTGTAGCC	335
OY	192	ctgcggyagacgtltagagagagagcaagggcttgcacagcccaaccaaacctgtgcgtcgc	251
Db	336	ATGCCCATAGGGCCAAATGATTTGGAATAATTACCTTTGTCTGCTGCTTGACTACCGAGATTTGC	395
OY	252	ctgcgcgaccccgctctcttcgcgcacgcgtgttctgtctltgtagagacatccgtgtccacc	311
Db	396	TTGGCCACCTTGACATGTTCCACAGTCTAAACGTACTCTGTGGCCCCCATAGCGGTGTCTGT	455
OY	312	tggttcgcggttgatltgccccgcgacccccagccagcaacaacagctgcaacgcgtcc	371
Db	456	GGGTGGGGGTGTGGGGAAGAAGGACAGAGACTGAGAGATGTGGCGTGAACGAGTGTGC	515
OY	372	cccaagcaacttctcaagccagcagctccagctcagagcagltgtccagaccaccaaccgcaacty	431
Db	516	TGCGGGTACCTTTCCAGATGTGCTCTTGTAGTGTATGTAATTCGAACGATTCACAGACTG	575
OY	432	caagcccttgagcctgtgcctccaatltgtgcagagctcttccctccatgaacacctgtgcac	491
Db	576	TCTGTGTACGAACCTGGGTGTGATCAACGCCGGGAGCCACAGAGACACAGACAACTGTGTGG	635
OY	492	caagctgacgtgctttccccctccagacc	549
Db	636	CACACTCCCGTCTTCTCCAGCTCCACC	663

RESULT 8  
 US-09-042-785A-24  
 ; Sequence 24, Application US/09042785A  
 ; Patent No. 6194151  
 ; GENERAL INFORMATION:  
 APPLICANT: Busfield, Samantha J  
 TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY  
 TITLE OF INVENTION: AND USES THEREFOR  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentln Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/042,785A  
 FILING DATE: 17-MAR-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/938,896  
 FILING DATE: 26-SEP-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E  
 REGISTRATION NUMBER: 36,1207  
 REFERENCE/DOCKET NUMBER: MEI-001CP  
 TELECOMMUNICATION INFORMATION:



RESULT 10  
US-09-042-785A-3  
Sequence 3, Application US/09042785A  
Patent No. 6194151  
GENERAL INFORMATION:  
APPLICANT: Busfield, Samantha J  
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,785A  
FILING DATE: 17-MAR-1998  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/938,896  
FILING DATE: 26-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MEI-001CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ. ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2612 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 190..951  
US-09-042-785A-3

Query Match 8.4%; Score 68; DB 4; Length 2612;  
Best Local Similarity 45.9%; Pred. No. 1.9e-05;  
Matches 233; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

QY 12 caccatccccctgacgagacagagagggagcgctgtgtgcccagtgcccc 71  
DB 345 CACATACCGCCCATGTGACCGTCCACCGCCAGGTCTTACCTGTACAGTGTCCAGC 404  
QY 72 aggcacacttggtgacgagcgctgtgcccgcgagacagccccaagcgtgtgtcc 131  
DB 405 AGGAACTTATGCTCTGATGATTGTACCAACACAGCGCTCGGGTGTGACAGATTGCC 464  
QY 132 accgcgcacactaacgacgagttctgtgaactacctgtgagcgctgtccactgtcaagtcct 191  
DB 465 TGTGGGACCTTTACCGAGGATGAGATGACATAGAGAAATGCCATGCTGACTGACGCC 524  
QY 192 ctgcgggagcgatgagagagcgacgaggtcttcacacgacccacaacgctgtccg 251  
DB 525 ATGCCCCATGGCCCATGTTTGAAGAAATTACCTTGTGCTGCTTGACCTGACCGAGATGCAC 584  
QY 252 ctgcgcacgagcgtcttcgacgacgctgtgtctgtctgttgagacgacgcatgtgtccac 311  
DB 585 TTGCCCCACCTGTGATGTTCCAGTCTAACGCTACTGTCGCCCATATGAGGTGTCTGT 644  
QY 312 tgtgtgcgagcgatgtatgtgccccggcaccaccagccagacagacgagtgccgctgtccc 371

DB 645 GCGTTGGAGGTGTGTCGGGAAGAAAGGACAGACATGACAGATGTGCGGTGTAAAGAGTGTGC 704  
QY 372 cccagcactcttcacgacccagctcagctcagagcagtgccagccccaactg 431  
DB 705 TCGGGGTACCTCTTCACATGATGGCTTCTAGTGTATGAAATGCAACATACACAGACTG 764  
QY 432 cagcgccctggcctgtgcccctcaatgtgcaagctcttcctccatgacccctgtgac 491  
DB 765 TCTGATGACAGAACTGTGTGATCAAGCGGAGACCAAGAGACAGACAAAGTGTGG 824  
QY 492 cagctgcacgagcttccccctcagcacc 519  
DB 825 CACACTCCCGTCTTTCACGCTCCACC 852

RESULT 11  
US-09-042-785A-22  
Sequence 22, Application US/09042785A  
Patent No. 6194151  
GENERAL INFORMATION:  
APPLICANT: Busfield, Samantha J  
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,785A  
FILING DATE: 17-MAR-1998  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/938,896  
FILING DATE: 26-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MEI-001CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ. ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2638 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 510..2327  
US-09-042-785A-22

Query Match 8.4%; Score 68; DB 4; Length 2638;  
Best Local Similarity 45.9%; Pred. No. 1.9e-05;  
Matches 233; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

QY 12 caccatccccctgacgagacagagagggagcgctgtgtgcccagtgcccc 71  
DB 665 CACATACCGCCCATGTGACCGTCCACCGCCAGGTCTTACCTGTGACAGTGTCCAGC 724  
QY 72 aggcacacttggtgacgagcgctgtgcccgcgagacagccccaagcgtgtgtccgctgtcc 131  
DB 725 AGGAACTTATGCTCTGATGATTGTACCAACACAGCGCTCGGGTGTGACAGATTGCC 784







APPLICATION NUMBER: US/08/458,298  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/209,747  
FILING DATE: 14-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1447-104P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2793 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Nephila clavipes  
TISSUE TYPE: minor ampullate gland  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 183..2675  
OTHER INFORMATION: /product= "N. clavipes minor  
OTHER INFORMATION: ampullate silk protein"  
US-08-458-298-1

Query Match 6.4%; Score 52; DB 1; Length 2793;  
Best Local Similarity 51.8%; Pred. No. 0.025;  
Matches 118; Conservative 0; Mismatches 110; Indels 0; Gaps 0;  
QY 553 gtcacgacttgcgttcacagacatctccatcaagagctgcagcgctgcag 612  
DB 1755 GTGCTGGAGCTGGAGCTGCTGACAGTGTGAGCTGAGCGCTGCAGTGCAGAGCAG 1814  
QY 613 gccctcagagcccgagggctggtgcgacacccaagggccgagcgcttcag 672  
DB 1815 GAGCTGGAGCTGAGCTGATGAGGTGATACGCTGCCGAGCAGAGAGCTGCTGCG 1874  
QY 673 ctgaagctgcgctgcgctcaaggaclctctggggcgaggaagcgctgcgtg 732  
DB 1875 CAGCTGCTGAGCAGAGCTGAGGCGCTGCGGCTTACAGTACAGAGTGGTGCAGAG 1934  
QY 733 cggctcgtcagcgctgcgctgagcagatgcccgggctgagcg 780  
DB 1935 CCGCTGGTGTGAGCTGAGCGCTGACAGTGCAGAGCAGAGAGCTG 1982

Search completed: November 2, 2001, 15:03:58  
Job time: 5589 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2001, 12:34:01 ; Search time 13.94 Seconds

(without alignments)  
443.121 Million cell updates/sec

Title: US-09-006-352-2

Perfect score: 1634  
Sequence: 1 MRALGPGLSLCLVLALPA.....RVARMPGLERSVERFLFVH 300

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/Backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1634	100.0	300	2	US-08-794-796-2
2	444	27.2	401	3	US-08-974-022-6
3	444	27.2	401	4	US-09-042-785A-12
4	425.5	26.0	401	3	US-08-974-022-2
5	424.5	26.0	401	3	US-08-974-022-2
6	424.5	26.0	401	4	US-09-042-785A-13
7	353.5	21.6	461	4	US-09-042-785A-7
8	351.5	21.5	461	1	US-08-385-229-2
9	351.5	21.5	461	2	US-08-650-000-2
10	351.5	21.5	461	4	US-08-477-347-3
11	351.5	21.5	461	6	5395760-2
12	346	21.2	227	3	US-08-974-022-48
13	344	21.1	486	1	US-08-243-010-1
14	344	21.1	518	1	US-08-385-229-4
15	332.5	20.3	474	2	US-08-650-000-4
16	332.5	20.3	474	4	US-09-042-785A-8
17	332.5	20.3	474	6	5395760-4
18	318	19.5	163	4	US-08-219-237B-5
19	318	19.5	163	4	US-08-477-347-13
20	316	19.3	164	2	US-08-232-087A-9
21	287	17.6	605	4	US-09-042-785A-4
22	287	17.6	605	4	US-09-042-785A-23
23	287	17.6	655	3	US-08-959-382-2
24	285.5	17.5	197	2	US-08-505-606-1
25	264.5	16.2	355	1	US-08-292-549-6
26	246	15.1	283	3	PCT-US86-12374-2
27	239	14.6	451	3	US-08-996-139-4

28	239	14.6	451	4	US-08-995-659-4	Sequence 4, App11
29	239	14.6	616	3	US-08-996-139-6	Sequence 6, App11
30	239	14.6	616	4	US-08-995-659-6	Sequence 6, App11
31	236.5	14.5	207	3	US-08-974-022-47	Sequence 47, App1
32	236.5	14.5	325	4	US-08-292-549-2	Sequence 2, App11
33	236.5	14.5	325	4	US-09-042-785A-9	Sequence 9, App11
34	236.5	14.5	325	5	PCT-US91-02207-2	Sequence 2, App11
35	235.5	14.4	591	4	US-08-995-659-2	Sequence 2, App11
36	235.5	14.4	625	3	US-08-996-139-15	Sequence 15, App1
37	233.5	14.3	625	4	US-08-995-659-15	Sequence 15, App1
38	233.5	14.3	625	4	US-08-147-784-2	Sequence 2, App11
39	226	13.8	277	2	US-08-195-967-2	Sequence 2, App11
40	226	13.8	277	4	US-09-042-785A-2	Sequence 2, App11
41	225	13.8	573	4	US-08-292-549-4	Sequence 4, App11
42	215	13.2	326	5	PCT-US91-02207-4	Sequence 4, App11
43	215	13.2	205	3	US-08-974-022-51	Sequence 51, App1
44	214	13.1	205	3	US-08-219-237B-8	Sequence 8, App11
45	212	13.0	139	2		

## ALIGNMENTS

RESULT 1  
US-08-794-796-2  
; Sequence 2, Application US/08794796  
; Patent No. 5885800  
; GENERAL INFORMATION:  
; APPLICANT: Emery, John  
; APPLICANT: Tan, KB  
; APPLICANT: Young, Alem  
; APPLICANT: Young, Peter  
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
; TITLE OF INVENTION: TR4  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/794,796  
; FILING DATE: 04-FEB-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Han, William T  
; REGISTRATION NUMBER: 34,344  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-4026  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 300 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-794-796-2  
Query Match 100.0%; Score 1634; DB 2; Length 300;

Best Local Similarity 100.0%; Pred. No. 1.8e-127;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGSLTCLVLPALPVPVAVGAETPTYPWRDAETGERLVCAQCPPTGVOR 60  
1 MRALEGSLTCLVLPALPVPVAVGAETPTYPWRDAETGERLVCAQCPPTGVOR 60  
Db 1 MRALEGSLTCLVLPALPVPVAVGAETPTYPWRDAETGERLVCAQCPPTGVOR 60  
QY 61 PCRRDPTTGGCPPTPHRYTOFWMYLERCRVCNVLGGEREERACHATNHRACRRTGFF 120  
61 PCRRDPTTGGCPPTPHRYTOFWMYLERCRVCNVLGGEREERACHATNHRACRRTGFF 120  
Db 61 PCRRDPTTGGCPPTPHRYTOFWMYLERCRVCNVLGGEREERACHATNHRACRRTGFF 120  
QY 121 AHAGFCLHNASCPGAGVIAFGTPTSONTOGCPGPGFFSASSSSSECCOHRNCTALGLA 180  
121 AHAGFCLHNASCPGAGVIAFGTPTSONTOGCPGPGFFSASSSSSECCOHRNCTALGLA 180  
Db 121 AHAGFCLHNASCPGAGVIAFGTPTSONTOGCPGPGFFSASSSSSECCOHRNCTALGLA 180  
QY 181 LNPVGSSTHDLCTSCGPFSTRVPGAECEBAVIDFVAFODISTKRLQALAEAP 240  
181 LNPVGSSTHDLCTSCGPFSTRVPGAECEBAVIDFVAFODISTKRLQALAEAP 240  
Db 181 LNPVGSSTHDLCTSCGPFSTRVPGAECEBAVIDFVAFODISTKRLQALAEAP 240  
QY 241 GKGPTPRAGALQILKRLTELGAQDGLLVRLQALVAVMPGLERSVRERLPVH 300  
241 GKGPTPRAGALQILKRLTELGAQDGLLVRLQALVAVMPGLERSVRERLPVH 300  
Db 241 GKGPTPRAGALQILKRLTELGAQDGLLVRLQALVAVMPGLERSVRERLPVH 300

## RESULT 2

US-08-974-022-6  
Sequence 6, Application US/08974022  
Patent No. 6015938  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehaviiland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022-6

Query Match 27.2%; Score 444; DB 3; Length 401;  
Best Local Similarity 39.6%; Pred. No. 3.4e-29;  
Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LCLVIALPALPVPVAVGAET--PTYPWRDAETGERLVCAQCPPTGVORCRDPT 68  
11 LCLVIALPALPVPVAVGAET--PTYPWRDAETGERLVCAQCPPTGVORCRDPT 68  
Db 4 LCLCAL---VFLDISIKMTTQETFPKYLHYDETSHTLDCDKPCPTGYLKHCHTAKMT 60

QY 69 TCGCPPTPHRYTOFWMYLERCRVCNVLGGEREERACHATNHRACRRTGFFAHAGFCL 128  
69 TCGCPPTPHRYTOFWMYLERCRVCNVLGGEREERACHATNHRACRRTGFFAHAGFCL 128  
Db 61 VCAPCPDHYTSDSMHSDCLCYSPYCKELOYVKQECNTHNRVCECKEGRLTEIEFCLK 120  
QY 129 HASCPCGAGVIAFGTPTSONTOGCPGPGFFSASSSSSECCOHRNCTALGLANVPGSSS 188  
129 HASCPCGAGVIAFGTPTSONTOGCPGPGFFSASSSSSECCOHRNCTALGLANVPGSSS 188  
Db 121 HNSCPGFCVVOAGTPTERTVCKRCPDGFSSMETSSKAPCRKHTNCSVGLLLTQKNAT 180  
QY 189 HDTLCTSCGPFSTRVPGAE--CERAVIDF 218  
189 HDTLCTSCGPFSTRVPGAE--CERAVIDF 218  
Db 181 HDNI---CGNSBSTQKCGIDVTLCEAFRR 209

## RESULT 3

US-09-042-785A-12  
Sequence 12, Application US/09042785A  
Patent No. 6194151  
GENERAL INFORMATION:  
APPLICANT: Bustfield, Samantha J  
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,785A  
FILING DATE: 17-MAR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/938,896  
FILING DATE: 26-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MET-001CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)742-4214  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: Internal  
US-09-042-785A-12

Query Match 27.2%; Score 444; DB 4; Length 401;  
Best Local Similarity 39.6%; Pred. No. 3.4e-29;  
Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LCLVIALPALPVPVAVGAET--PTYPWRDAETGERLVCAQCPPTGVORPCRRDPT 68  
11 LCLVIALPALPVPVAVGAET--PTYPWRDAETGERLVCAQCPPTGVORPCRRDPT 68  
Db 4 LCLCAL---VFLDISIKMTTQETFPKYLHYDETSHTLDCDKCPGTYLKHCHTAKMT 60  
QY 69 TCGCPPTPHRYTOFWMYLERCRVCNVLGGEREERACHATNHRACRRTGFFAHAGFCL 128  
69 TCGCPPTPHRYTOFWMYLERCRVCNVLGGEREERACHATNHRACRRTGFFAHAGFCL 128  
Db 61 VCAPCPDHYTSDSMHSDCLCYSPYCKELOYVKQECNTHNRVCECKEGRLTEIEFCLK 120  
QY 129 HASCPCGAGVIAFGTPTSONTOGCPGPGFFSASSSSSECCOHRNCTALGLANVPGSSS 188  
129 HASCPCGAGVIAFGTPTSONTOGCPGPGFFSASSSSSECCOHRNCTALGLANVPGSSS 188  
Db 121 HNSCPGFCVVOAGTPTERTVCKRCPDGFSSMETSSKAPCRKHTNCSVGLLLTQKNAT 180



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? COUNTRY: USA
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/042,785A
? FILING DATE: 17-MAR-1998
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/938,896
? FILING DATE: 26-SEP-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Mandragoras, Amy E
? REGISTRATION NUMBER: 36,207
? REFERENCE/DOCKET NUMBER: MEI-001CP
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617)227-7400
? TELEFAX: (617)742-4214
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 401 amino acids
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? FRAGMENT TYPE: Internal
? US-09-042-785A-13

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Query Match          26.0%; Score 424.5; DB 4; Length 401;
Best Local Similarity 39.0%; Pred. No. 1.4e-27;
Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;

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QY 34 PTVMRDETERLVCAACPPGPTGVORPCRRDPTTCGCPPEPHYTOFWNVLERCRCNV 93
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DB 26 PKYLHYDETHOLLOKCAPGTGLKONCHYRKRTLCVPCPDHSYTDSSWHTSDSCVYCS 85
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 94 LCGREERARACHMTNHNACRGTFEFHAGCELEHASCPRGAGVIAAGTSONTOGCP 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86 VCKELQSVKOCNCRTHNVCCEGRYIEFECLKHNSCPGSGVQAGTERTVCKKC 145
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 154 PPGTFSSASSSECOQPHRNCTALGLALNVGSSSHDTLCTSCGFLSTRVPAER--C 211
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 146 PDGFGSGTSSKAPCIKHTNCTGLLLIQKNAHDNV--CSGNREATQKCGIDVTL 202
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 212 ERAVIDEYAFODISIKRLQLAL 236
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 203 EEAFFRFVAPRKIIPLNLSLVLSL 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

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RESULT 7
? US-09-042-785A-7
? Sequence 7, Application US/09042785A
? Patent No. 6194151
? GENERAL INFORMATION:
? APPLICANT: Busfield, Samantha J
? TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
? NUMBER OF SEQUENCES: 31
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: LAHIVE & COCKFIELD, LLP
? STREET: 28 State Street
? CITY: Boston
? STATE: Massachusetts
? COUNTRY: USA
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:

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? APPLICATION NUMBER: US/09/042,785A
? FILING DATE: 17-MAR-1998
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/938,896
? FILING DATE: 26-SEP-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Mandragoras, Amy E
? REGISTRATION NUMBER: 36,207
? REFERENCE/DOCKET NUMBER: MEI-001CP
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617)227-7400
? TELEFAX: (617)742-4214
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 461 amino acids
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? FRAGMENT TYPE: Internal
? US-09-042-785A-7

```

```

Query Match          21.6%; Score 353.5; DB 4; Length 461;
Best Local Similarity 29.8%; Pred. No. 1.2e-21;
Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;

```

```

QY 8 GLSLICLVLPALPLPVAAGVAFETPTYPWRDAETGE-----RLVCAACPPG 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 13 GLELMAAHLPA-----QVAFETPYAP---EPGSTCRLEYYDQTAQMCSCSKSPG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 56 TVOORPCRRDPTTCGCPPEPHYTOFWNVLERCRCNVLCGEEERARACHATNHRACRC 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 QHAKVFCTKTSIDVCCSCDESTYTOLMNVPECLTSGSCSSDQVETQACTREQNNITC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 116 RTGFEHAG-----FLEHASCPRGAGVIAAGTSONTOGCPGPTFSASSSECO 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 RPYWYCALMSQECRCALPKRCRPGVARKPTETISDVVCKKACAGCTTSNTTSSDIDR 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 PHNCTALGLALNVGSSSHDTLCTSCGFLSTRVPAEERAVIDYVAODISIKRL 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 PHQICNVVA-----TFGASDAVCTST--PTRMAFGVHLDPV-----STRSQT 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 QRLQLALEPE-----GWCPTPRA---GRAIQLKLRRLTELLGADQCALVRLQL 280
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 228 QPTPEPSTAFSTFLLPMGSPSPAESGTGDFALPGLVGVITAL-----GLIIGVNCV 282
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 281 ---RVARMP-GLERSVREPLP 298
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 IMTVKKKKPLCLQREAKVPLP 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 8
? US-08-385-229-2
? Sequence 2, Application US/08385229
? Patent No. 5605690
? GENERAL INFORMATION:
? APPLICANT: Jacobs, Cindy A.
? TITLE OF INVENTION: Method of Treating TNF-Dependent
? NUMBER OF SEQUENCES: 5
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Immunex Corporation
? STREET: 51 University Street
? CITY: Seattle
? STATE: Washington
? COUNTRY: U.S.A.
? ZIP: 98101
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,229
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,236
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wright, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 587-0606
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-385-229-2
```

```

Query Match      21.5%; Score 351.5; DB 1; Length 461;
Best Local Similarity 29.8%; Pred. No. 1.7e-21;
Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;
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```

QY 8 GLSLCLLVLPALPLPVPVAVGVAETPTVPMWDAETGE-----RLVCAOCPG 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 13 GLELMAAHLPA-----QVAFTPYAP---EPGSTRLEREYDQTAOMCCSKSPG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 56 TVQORPCRDSPPTGCPGPRHYTOFWNYLERGCYCNVLGGEREEARACHATHNRARC 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 QHAKVFCTKTSIVDCSCEDSTYTQLNMWVPECLSCGSCSSDOVEQTACTRQNRIC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 116 RTGFFAHAG-----FCLHASCPPGAGVIAPGTPSONTOCQPCPGTFSASSSSSEQ 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 RPYWCALSKQEGRLCAPLRKCRPGFGVARPGTETSDVYCKPCAPGTFSTNTSSD 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 PHRNCTALGLALNVPSSSHDTLCTSGTGFPLSTRVPGAECECERAVIDEVAFD 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 PHQICNVVA-----IPGNASDAVCTSTS--PTSMAPGAVHLQPV-----ST 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 QRLQLALEPE-----GWCPTPRA---GRAALQKLRRRLTELGADGALLVRLQAL 280
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 228 QPTPEPSTAPSTSFLLPMGSPPEAGSTGDFALPVGLIVGTAL-----GLLI 282
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 281 ---RVARMP-GLERSVREFLP 298
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 IMQVKKKKPLCLQREAKVPHLP 304
```

```

RESULT 9
; US-08-650-000-2
; Sequence 2, Application US/08650000
; Patent No. 5945397
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,000
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,453
; FILING DATE:
; APPLICATION NUMBER: US/08/038,765
; FILING DATE:
; APPLICATION NUMBER: US 403,241
; FILING DATE: 05-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 405,370
; FILING DATE: 11-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 421,417
; FILING DATE: 13-OCT-1989
; APPLICATION DATA:
; APPLICATION NUMBER: US 523,635
; FILING DATE: 10-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wright, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2501-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-650-000-2
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```

Query Match      21.5%; Score 351.5; DB 2; Length 461;
Best Local Similarity 29.8%; Pred. No. 1.7e-21;
Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;
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```

QY 8 GLSLCLLVLPALPLPVPVAVGVAETPTVPMWDAETGE-----RLVCAOCPG 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 13 GLELMAAHLPA-----QVAFTPYAP---EPGSTRLEREYDQTAOMCCSKSPG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 56 TVQORPCRDSPPTGCPGPRHYTOFWNYLERGCYCNVLGGEREEARACHATHNRARC 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 QHAKVFCTKTSIVDCSCEDSTYTQLNMWVPECLSCGSCSSDOVEQTACTRQNRIC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 116 RTGFFAHAG-----FCLHASCPPGAGVIAPGTPSONTOCQPCPGTFSASSSSSEQ 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 RPYWCALSKQEGRLCAPLRKCRPGFGVARPGTETSDVYCKPCAPGTFSTNTSSD 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 PHRNCTALGLALNVPSSSHDTLCTSGTGFPLSTRVPGAECECERAVIDEVAFD 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 PHQICNVVA-----IPGNASDAVCTSTS--PTSMAPGAVHLQPV-----ST 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 QRLQLALEPE-----GWCPTPRA---GRAALQKLRRRLTELGADGALLVRLQAL 280
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 228 QPTPEPSTAPSTSFLLPMGSPPEAGSTGDFALPVGLIVGTAL-----GLLI 282
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 281 ---RVARMP-GLERSVREFLP 298
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 IMQVKKKKPLCLQREAKVPHLP 304
```

```

RESULT 10
; US-08-477-347-3
; Sequence 3, Application US/08477347
; Patent No. 6232446
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
```

```

? APPLICANT: BELETSKY, Igor
? TITLE OF INVENTION: TNF LIGANDS
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: BROWDY AND NEIMARK
? STREET: 419 Seventh Street, N.W.
? CITY: Washington
? STATE: D.C.
? COUNTRY: USA
? ZIP: 20004
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/477,347
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/115,685
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: IL 106271
? FILING DATE: 08-JUL-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Townsend, G. Kevin
? REGISTRATION NUMBER: 34,033
? REFERENCE/DOCKET NUMBER: WALLACH-10
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-628-5197
? TELEFAX: 202-737-3528
? TELEX: 248633
? INFORMATION FOR SEQ. ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 461 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-477-347-3
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Query Match      21.5%  Score 351.5; DB 4; Length 461;
Best Local Similarity 29.8%; Pred. No. 1.7e-21;
Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;

QY 8 GSLGLCLVIALPALLPVAVRGVAETPTYPWRDAETGE-----RLVCAQCPCPG 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 13 GLELMAAALPA-----QVAFTPYAP-----EPGTCRLREYYDOTAQMCCKSPG 60

QY 56 TVQVRCRRSDPTGCPRPRIHYTOFWNYLERGRCYCNVLCGEEREARACHATHNRACRC 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 QHAKVFCTKTSDFVCDSCEDSTYTQLMNWPBCLSCGSCSSSDQVETQACTRQNRICTC 120

QY 116 RTGFEFAHAG-----FCLHASCPPGAGVIAPGTPSONTCQCPPTGFSASSSSSEDCQ 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 RFGWYCALSKQEGRCIAPLRKCRPGFVGARPGTETSDVYCKRCACGTETNTSIDICR 180

QY 170 PHRNCYALGLALNWPSSSHDTICTSGTGPLSTRVPGAEECCERAVIDFAFDISIKRL 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 PHQICNVVA-----IPGNASMDAVCTSTS--PTRSMAPGAVHLPGPV-----STRSQHT 227

QY 230 QRLQLALEAPE-----GWSPTPRA-----GRAALQKLRRRLTELGAODGALLVRLQAL 280
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 228 QPTPEPSTAPSTSFLLPMGSPSPAEGSTGDFALPVGLIVGTAL-----GLIITGVNVCV 282

QY 281 ---RVARMP-GLERSVREERFLP 298
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 IMTVKKRKLCLQREAKVPHLP 304
```

RESULT 11

```

5395760-2
? Patent No. 5395760
? APPLICANT: SMITH, CRAIG A.; GODWIN, RAYMOND G.; BECKMANN,
? M. PATRICIA
? TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
? B-RECEPTORS
? NUMBER OF SEQUENCES: 17
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/523,635
? FILING DATE: 10-MAY-1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 421,417
? FILING DATE: 13-OCT-1989
? APPLICATION NUMBER: 405,370
? FILING DATE: 11-SEP-1989
? APPLICATION NUMBER: 403,241
? FILING DATE: 05-SEP-1989
? SEQ. ID NO: 2
? LENGTH: 461
5395760-2
```

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Query Match      21.5%  Score 351.5; DB 6; Length 461;
Best Local Similarity 29.8%; Pred. No. 1.7e-21;
Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;

QY 8 GSLGLCLVIALPALLPVAVRGVAETPTYPWRDAETGE-----RLVCAQCPCPG 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 13 GLELMAAALPA-----QVAFTPYAP-----EPGTCRLREYYDOTAQMCCKSPG 60

QY 56 TVQVRCRRSDPTGCPRPRIHYTOFWNYLERGRCYCNVLCGEEREARACHATHNRACRC 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 QHAKVFCTKTSDFVCDSCEDSTYTQLMNWPBCLSCGSCSSSDQVETQACTRQNRICTC 120

QY 116 RTGFEFAHAG-----FCLHASCPPGAGVIAPGTPSONTCQCPPTGFSASSSSSEDCQ 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 RFGWYCALSKQEGRCIAPLRKCRPGFVGARPGTETSDVYCKRCACGTETNTSIDICR 180

QY 170 PHRNCYALGLALNWPSSSHDTICTSGTGPLSTRVPGAEECCERAVIDFAFDISIKRL 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 PHQICNVVA-----IPGNASMDAVCTSTS--PTRSMAPGAVHLPGPV-----STRSQHT 227

QY 230 QRLQLALEAPE-----GWSPTPRA-----GRAALQKLRRRLTELGAODGALLVRLQAL 280
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 228 QPTPEPSTAPSTSFLLPMGSPSPAEGSTGDFALPVGLIVGTAL-----GLIITGVNVCV 282

QY 281 ---RVARMP-GLERSVREERFLP 298
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 IMTVKKRKLCLQREAKVPHLP 304
```

```

RESULT 12
US-08-974-022-48
? Sequence 48, Application US/08974022
? Patent No. 6015938
? GENERAL INFORMATION:
? APPLICANT: Boyle, William J.
? APPLICANT: Lacey, David L.
? APPLICANT: Calzone, Frank J.
? APPLICANT: Chang, Ming-Shi
? TITLE OF INVENTION: OSTEOPROTEGERIN
? NUMBER OF SEQUENCES: 33
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Amgen Inc.
? STREET: 1840 Dehaven Drive
? CITY: Thousand Oaks
? STATE: California
? COUNTRY: USA
? ZIP: 91320-1789
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
```





```

: TELEPHONE: (206) 587-0430
: TELEFAX: (206) 587-0606
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 518 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-385-229-4

```

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Query Match      21.1%; Score 344; DB 1; Length 518;
Best Local Similarity 33.8%; Pred. No. 8e-21;
Matches: 74; Conservative 28; Mismatches 81; Indels 36; Gaps 6;

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```

QY 8 GLSLICLVLPALPYPAVAVGAEPTPYWDAETGE-----RLVCAACPPG 55
Db 42 GLELMAAHLPA-----QVAETPYAP---EPGSTRLREYDQTMCCSKCPG 89
QY 56 TEVQRCRDSPTTCGCPRHHTQFWNYLERCRYCNVLCGEREEARACHATHNRACRC 115
Db 90 QHAKVFCTKTSIDVCDSCEDSTYQLNWNVPECLSCGSCSDQVETQACTREONRICTC 149
QY 116 RTGFFAHAG-----FLEHNASCPGAGVIAFGTSPONTQOCPCPGPTGSASSSSSQ 169
Db 150 RFGVYCAALSKOEGCRICAPLRKCRPGFVARPGTETSDVYCKPCAPGTFSTNTSIDI 209
QY 170 PHRNCTALGLALNVPSSSHDTLCTSCGTGFPPLSTRVPGA 208
Db 210 PHQICNVVA---IPGNASMDAVCTSTS--PTRSMAPGA 242

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RESULT 15

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US-08-650-000-4
: Sequence 4, Application US/08650000
: Patent No. 5945397
: GENERAL INFORMATION:
:   APPLICANT: Smith, Craig A.
:   APPLICANT: Goodwin, Raymond G.
:   TITLE OF INVENTION: Tumor Necrosis Factor Receptors
:   NUMBER OF SEQUENCES: 4
:   CORRESPONDENCE ADDRESS:
:     ADDRESS: Immunex Corporation
:     STREET: 51 University Street
:     CITY: Seattle
:     STATE: Washington
:     COUNTRY: U.S.A.
:     ZIP: 98101
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Patent Release #1.0, Version #1.25
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/650,000
:     FILING DATE:
:     CLASSIFICATION: 435
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US/08/468,453
:       FILING DATE:
:       APPLICATION NUMBER: US/08/038,765
:       FILING DATE:
:       APPLICATION NUMBER: US 403,241
:       FILING DATE: 05-SEP-1989
:       PRIOR APPLICATION DATA: US 405,370
:       FILING DATE: 11-SEP-1989
:       PRIOR APPLICATION DATA: US 421,417
:       FILING DATE: 13-OCT-1989
:       PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US 523,635

```

```

: FILING DATE: 10-MAY-1990
: ATTORNEY/AGENT INFORMATION:
:   NAME: Wright, Christopher L.
:   REGISTRATION NUMBER: 31,680
:   REFERENCE/DOCKET NUMBER: 2501-D
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: (206) 587-0430
:     TELEFAX: (206) 233-0644
:   INFORMATION FOR SEQ ID NO: 4:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 474 amino acids
:       TYPE: amino acid
:       TOPOLOGY: linear
:     MOLECULE TYPE: protein
:   US-08-650-000-4

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Query Match      20.3%; Score 332.5; DB 2; Length 474;
Best Local Similarity 29.7%; Pred. No. 6.4e-20;
Matches: 81; Conservative 44; Mismatches 109; Indels 39; Gaps 9;

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QY 46 RLVCAACCPOTFEVQRCRDSPTTCGCPRHHTQFWNYLERCRYCNVLCGEREEARAC 105
Db 52 QMCCACCPQGYVYKHCNKTSDIVCADCEASMTQYVNOFRICLSCSSCTDQYEIRAC 111
QY 106 HATHNRACRGTGFF---AHAGF---CLEHNASCPGAGVIAFGTSPONTQOCPCPGTF 158
Db 112 TKOONRVACAEAGRYCALKTHSGCRQCRRLSKCPGFGVASSRAPNGVLCACAPGTF 171
QY 159 SASSSSEOCOPRNRCTALGLALNVPSSSHDTICT---SCTGFPPLSTRVPGAEECERA 214
Db 172 SDTTSSTDCRPHRISILA---IPGNASTDAVCAPESTPLSAIPRTIYVSQPEPTRSQ 227
QY 215 VIDEFAFODISTKRLORLOALEAPGNGPTP-----RACRAALQKLRRTELIGAD 269
Db 228 PLD-----QERGPGQTSILSL-----GSTPIEDSTGGISLPLGLIVGYTSL----- 272
QY 270 GALLVRLLOAL-----RYAKMPGLERSVREERFLP 298
Db 273 GLMLGLVNCIIIVORKKRPSCLOKDAKVPVHP 305

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Search completed: October 31, 2001, 12:39:06  
 Job time: 305 sec



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117 eCysLeuYHisArgSerCysProGlyPheGlyValGlnAlaG 134
449 GCACCCCGACGACGACGACGACGACGACGACGACGACGACGAC 498
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134 LyrHrProGlnArgAsnThrValCysLysArgCysProAspLysPhe 150
499 TCAGCCAGCAGCTCCAGCTCCAGCAGCAGCAGCAGCAGCAGCAG 548
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151 SerAsnGlnThrSerSerLysAlaProCysArgLysHisThrAsn 167
549 GCGCCCTGGGCTGGCCCTCAATGTGCCAGGCTCTTCCCATGACAC 598
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167 rValPheGlyLeuLeuLeuThrGlnLysGlyAsnAlaThrHisAsp 184
599 TGTGACACAGCTGCACGTGGCTTCCCTCAGCAGCAGCAGGTTAC 648
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184 Le.....CysSerGlyAsnSerGlnSerThrGlnLysCysGly 197
649 GAGGAG.....TGTGACGCTGCCGCTCATGCACCTT 678
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198 AspValThrLeuCysGlnGlnAlaLapheArgPhe 209
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seq_documentation_block:
; Sequence 12, Application US/09042785A
; Patient No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; US-09-042-785a-12

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alignment_scores:
Quality: 444.00      Length: 212
Ratio: 3.194        Gaps: 4
Percent Similarity: 65.566      Percent Identity: 39.623

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alignment_block:
US-09-006-352-1 x US-09-042-785a-12
Align seg 1/1 to: US-09-042-785a-12 from: 1 to: 401

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55 CTGCTGCTCTGGTGTGGCGCTGCGCTGCTGCTGCTGCGCGCTGT 104
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4 LeuLeuCysAlaLeu.....ValPheLeuAspLysSerIleLeu 17
105 ACCCGAGATGCGAGAAACA.....CCACCTACCCCTGGCGGACG 148
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17 strThrThrGlnGlnThrPheProProLysThrLysThrAspGln 34
149 AGACAGGAGAGCGCTGTGTGTCGCGCAGTGCAGCGCCGACGCT 198
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34 LyrHrSerHisGlnLeuLeuCysAspLysCysProProGlyThrLys 50
199 CAGCGCGCTGCGCGCGCGAGACAGCCGACGAGCTGTGCGCTG 248
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51 LysGlnHisCysThrAlaLysThrLysThrValCysAlaProCys 67
249 GCGCCACTACAGCAGCTTGTGGACTACCTGAGCGCTGCGCTACT 298
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299 ACGTCTCTGCGCGGAGCGCTGAGAGAGAGGACGCGCTTGGCAG 348
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349 CACAACGCTGCTGCGCTGCGCGCAGCAGCGCTTCTTGGCGAGCT 398
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399 CTGCTGGAGACGACATGTGTCCACTGTGCGCGCGCTGATGCC 448
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599 TGTGACACAGCTGCACGTGGCTTCCCTCAGCAGCAGCAGGTTAC 648
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184 Le.....CysSerGlyAsnSerGlnSerThrGlnLysCysGly 197
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seq_name: /cgn2_6/ptodata/2/iaa/6a_comb.pep:us-08-974-022-2
seq_documentation_block:
; Sequence 2, Application US/08974022
; Patient No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive

```

CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022-2

alignment\_scores:  
Quality: 425.50 Length: 205  
Ratio: 3.199 Gaps: 2  
Percent Similarity: 64.878 Percent Identity: 39.512

Alignment\_block:  
US-09-006-352-1 x US-08-974-022-2 ..

Align seg 1/1 to: US-08-974-022-2 from: 1 to: 401

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42 PLYscysAlaProgluThrtyrleuLysGlnHisCysThrValArgArgL 59
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224 CCACGACGTGTGCGCGCTGTCCACCGCGGACGACGACGATTCGGAAC 273
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59 ysthrleuCyValProCysProAspTyrSerTyrThrAspSerTyrPrls 75
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274 TACCTGGAGCGCTCCGCTACTGCACAGCTCCTCGCGGAGCGCTGAGCA 323
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76 ThrsrAspGluCysValTyrCysSerProValCysLysGluLeuGlnTh 92
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324 GGAGGCGGAGCTCCGCGGACGACGACGCGCTGCGCGGCGCGCA 373
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92 rValylGlnGluCysAsnArgThrHisAsnArgValCysGluCysGluG 109
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374 CCGGCTCTTCGCGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 423
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109 LuGluArgTyrLeuGlnLeuGluPheCysLeuLysHisAspSerCysPro 125
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424 CCTGGTCCGCGGATTCGCGGACGCGGACGCGGACGCGGACGCGAGTG 473
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126 ProgluLeuLysValLeuGlnAlaGluTyrProgluArgGlnHisValCy 142
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474 CCAAGCCTGCGCGGACGCTTTCGACGACGACGACGCTGCTGCTGCTGAGC 523
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142 slAspArgCysProAspArgLysPheSerGluGluThrSerSerLysLar 159
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524 AGTCGACGCGGACGCGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 573
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159 rocysArgLysHisThrAsnCySerSerSerLeuLeuLeuLeuGln 175
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574 CCAAGCTCTCTCCATGACACCCCTGTGCACACGCTGACCTGCTGCC 623
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176 LysGluAsnAlaThrHisAspAsnVal.....CysSerGluAsnArg 189
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
624 CCTCAGACACGAGTACGACGAGTACGAG.....TGTGAGCGTGGCG 667
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
189 gGluAlaThrGlnAsnCyGlyLeuAspValThrLeuCyGluGluAlaP 206
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
668 TCATGACCTTGTGGCTTTCGAGACATCTCCATCAAGAGGCTGACGGG 717
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
206 hePheArgPheAlaValProThrLysIleLeuProAsnThrLeuSerVal 222
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
718 CTGCTGACGCGCGCTC 732
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
223 LeuValAspSerLeu 227
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seq\_name: /cgn2\_6/ploddata/2/iaa/6a\_COMB.pep:US-08-974-022-4

seq\_documentation\_block:  
Sequence 4, Application US/08974022

Patent No. 6015938

GENERAL INFORMATION:  
APPLICANT: Boyle, William J.

APPLICANT: Lacey, David L.

APPLICANT: Calzone, Frank J.

APPLICANT: Chang, Ming-Shi

TITLE OF INVENTION: OSTEOPROTEGERIN

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.

STREET: 1840 Dehavenland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022

FILING DATE: 12-DEC-1995

CLASSIFICATION:  
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/577,788

FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-378

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:

LENGTH: 401 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-974-022-4

alignment\_scores:  
Quality: 424.50 Length: 205  
Ratio: 3.144 Gaps: 2  
Percent Similarity: 65.854 Percent Identity: 39.024

Alignment\_block:  
US-09-006-352-1 x US-08-974-022-4 ..

Align seg 1/1 to: US-08-974-022-4 from: 1 to: 401

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26 ProlustylleuNH1tyrAspProgluThrGluAlaGlnleuLeuCyAs 42
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224 CCAGACACGTGGCCCGTGTCCACCGCCGACATACAGCAGCTTCGAGAC 273
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59 yStHleuGlnGlyValProCysProAspHisSerTyrThrAspSerTrpHis 75
    ||| ||| |||||::: |||||::: |||||::: |||||:::
274 TACSTGAGACGCTGCGCTACTGACAGCTCTGTGCGGAGACGCTGAGGA 323
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76 ThrSerArgLysValTyrCysSerProValCysLysGlnLeuGlnSe 92
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324 GGAGGACGGGCTTGCCAGCGCCACGACACGCTGCGCCGCTGCGGCA 373
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92 rValLysGlnGlyCysAsnArgThrHisAsnArgValCysGlnCysGlnG 109
    ||| ||| |||||::: |||||::: |||||::: |||||:::
374 CCGGCTTCTGCGGACGCGCTTGTCTGTGACAGCAGCAGCTGCTGCA 423
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109 LngLArgTyrLeuGlnLueGlnPheCysLeuYlHisArgSerCysPro 125
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424 CCGTGGTGGCGGCTGATGTCGCGCGGACGCGCCGACGACGACGAGTG 473
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126 ProGlySerGlyValAlaGlnAlaGlyThrProGlnArgAsnThrValCy 142
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474 CCAGCGCTGCGCCCGGACGACGCTTGTGACGACGAGCTGACGCTGAGAGC 523
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142 sLysLysCysProAspArgLysPhePheSerGlyGlnThrSerSerLysAla 159
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524 AGTGCACGCGCCGACGACGCTGCGCGCTGCGCGCTGCGCGCTGCAATG 573
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159 rOcysLLeuYlHisThrAsnCysSerThrPheGlyLeuLeuLeuGln 175
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574 CCAGCGCTTCTGCGGACGACGCTTGTGACGACGAGCTGAGCTGCTGCC 623
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176 LysGlyAsnAlaThrHisAspAsnVal.....CysSerGlyAsnArg 189
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624 CCGTACGACGAGCTGACGAGCTGAGAG.....TGTGAGCTGCCG 667
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189 gLValAlaThrGlnLysCysGlyLeaSprValThrLeuCysGlnGlnAla 206
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668 TCAATGACATTTGTGCTTCCAGGACATCTGCATGAAGAGCTGACGAGG 717
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206 hPheArgPheAlaValProThrLysLLeuLeuProAsnTrpLeuSerVal 222
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718 CTGCTGACGCGCTC 732
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seq_name: /cgn2_6/prodata/2/1aa/6b_COMB.pep:us-09-042-785A-13
seq_documentation block:
; Sequence 13: Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A

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; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; US-09-042-785A-13

alignment_scores:
    Quality: 424.50      Length: 205
    Ratio: 3.144        Gaps: 2
    Percent Similarity: 65.854    Percent Identity: 39.024

alignment_block:
US-09-006-352-1 x US-09-042-785A-13

Align seq 1/1 to: US-09-042-785A-13 from: 1 to: 401

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174 CCAGTGGCCCCCAGGACACCTTTGTGACAGCGCGCGCGCGCGCGAGAC 223
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42 pLysGlyAlaProGlyThrTyrLeuYlGlnHisCysThrValAlaArgL 59
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224 CCAGACGCTGCGCGCTGTCACGCGCGGACGCTGACGAGCTTGTGAGAC 273
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59 yStHleuGlnGlyValProCysProAspHisSerTyrThrAspSerTrpHis 75
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274 TACSTGAGACGCTGCGCTACTGACAGCTCTGTGCGGAGACGCTGAGGA 323
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76 ThrSerArgLysValTyrCysSerProValCysLysGlnLeuGlnSe 92
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324 GGAGGACGGGCTTGCCAGCGCCACGACACGCTGCGCCGCTGCGGCA 373
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92 rValLysGlnGlyCysAsnArgThrHisAsnArgValCysGlnCysGlnG 109
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142 sLysLysCysProAspArgLysPhePheSerGlyGlnThrSerSerLysAla 159
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159 rOcysLLeuYlHisThrAsnCysSerThrPheGlyLeuLeuLeuGln 175
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574 CCAGCGCTTCTGCGGACGACGCTTGTGACGACGAGCTGAGCTGCTGCC 623
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176 LysGlyAsnAlaThrHisAspAsnVal.....CysSerGlyAsnArg 189
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seq\_documentation\_block:

Sequence 7, Application US/09042785A  
 Patent No. 6194151  
 GENERAL INFORMATION:  
 APPLICANT: Buxfield, Samantha J  
 TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY  
 TITLE OF INVENTION: AND USES THEREFOR  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/042,785A  
 FILING DATE: 17-MAR-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/938,896  
 FILING DATE: 26-SEP-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragoras, Amy E  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: MEI-001CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)742-4214  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 461 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 US-09-042-785A-7

alignment\_scores:

Quality: 357.00 Length: 334  
 Ratio: 1.994 Gaps: 13  
 Percent Similarity: 53.593 Percent Identity: 29.940

alignment\_block:  
 US-09-006-352-1 x US-09-042-785A-7 ..

Align seg 1/1 to: US-09-042-785A-7 from: 1 to: 461

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 60 GTCCTGCTGGGCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 109  
 17 pAlaAlaAlaHisAlaLeuProAla.....G 26

110 GAGTGCAGAAAGACCCACTACCTGCGGAGGACGACAGACAGGAGG 159  
 26 InValAlaPheThrProTyrAlaPro.....GluProGlySer 38  
 160 .....CGCGTGTGTGCC 173  
 39 ThrCysArgLeuAlaGlyTyrTyrAspGlnThrAlaGlnMetCysCys 55  
 174 CCAGTGCCTCCCGAGGACCTTGTGACAGGCGCGCTGCCCGCAGAC 223  
 55 TlyScySerProGlyGlnHisAlaLysValPheCysThrThrSerA 72  
 224 CCAGCAGCTGTGCGCGCTGTCACCGCGCCACTACAGCAGCTTGAG 273  
 72 SpThrValCysAspSerCysGlnAspSerThrTyrThrGlnLeuTrp 88  
 274 TACCTGAGCGCTGCCCTACTGACAGCTCCTGCGGAGGAGCTGAGA 323  
 89 TrpValProGlyLysSerCysGlySerArgCysSerSerAspGln 105  
 324 GAGGACAGGCGCTTGCACGCCACACCAACAGCTGCGCGCTGCCGA 373  
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 374 CGCGCTTCTGCGCGCTGCT.....TTCGCTTG 405  
 122 roGlyTrpTyrCysAlaLeuSerLysGlnGluGlyCysArgLeuCy 138  
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 456 CAGCAGACAGCAGCGCGCGCTGCGCGCGCGCGCGCGCTGCGCG 505  
 155 uThrSerAspValValCysLysProCysAlaProGlyThrSerAs 172  
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 272 ...GlyLeuLeuIleIleGlyValAlaAsnValAlaMetThrGln 287  
 870 GCGCAGAGTGCCT...GCGTGAAGCGAGCGTCCGTGAGCGCTCTCC 916  
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seq\_documentation\_block:

Sequence 2, Application US/08385229

Patent No. 5605690

GENERAL INFORMATION:

APPLICANT: Jacobs, Cindy A.

APPLICANT: Smith, Craig A.

TITLE OF INVENTION: Method of Treating TNF-Dependent

NUMBER OF SEQUENCES: 5 Inflammation Using Tumor Necrosis Factor Antagonists

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentlin Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/385,229

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/946,236

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Wright, Christopher L.

REGISTRATION NUMBER: 31,680

REFERENCE/DOCKET NUMBER: 2503

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 587-0606

INFORMATION FOR SEQ. ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 461 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-385-229-2

alignment\_scores:

Quality: 355.00

Ratio: 1.994

Percent Similarity: 53.293

Percent Identity: 29.940

alignment\_block:

US-09-006-352-1 x US-08-385-229-2

Align seg 1/1 to: US-08-385-229-2 from: 1 to: 461

10 GCTCCAGACAGACCATGAGGCGCTGAGGCGCAGGCTGTGCTGCT 59  
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2 AAlaProValAlaValTrpAlaAlaLeu...AlaValGlyLeuGluLeuTr 17  
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17 PAlaAlaAlaHisAlaLeuProAla.....G 26  
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26 InValAlaPheThrProTyrAlaPro.....GluProGlySer 38  
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226 HisThrGlnProThrProGlnProSerThrAlaProSerThrSerPhe 242  
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seq\_documentation\_block:

Sequence 2, Application US/08650000  
 Patent No. 5945397  
 GENERAL INFORMATION:  
 APPLICANT: Smith, Craig A.  
 APPLICANT: Goodwin, Raymond G.  
 APPLICANT: Beckmann, M. Patricia  
 TITLE OF INVENTION: Tumor Necrosis Factor Receptors  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: U.S.A.  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/650,000  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/468,453  
 FILING DATE:  
 APPLICATION NUMBER: US/08/038,765  
 FILING DATE:  
 APPLICATION NUMBER: US 403,241  
 FILING DATE: 05-SEP-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 405,370  
 FILING DATE: 11-SEP-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 421,417  
 FILING DATE: 13-OCT-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 523,635  
 FILING DATE: 10-MAY-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Wight, Christopher L.  
 REGISTRATION NUMBER: 31,680  
 REFERENCE/DOCKET NUMBER: 2501-D  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 587-0430  
 TELEFAX: (206) 233-0644  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 461 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-650-000-2

alignment\_scores:  
 Quality: 355.00 Length: 334  
 Ratio: 1.994 Gaps: 13  
 Percent Similarity: 53.293 Percent Identity: 29.940

alignment\_block:

US-09-006-352-1 x US-08-650-000-2 ..  
 Align seg 1/1 to: US-08-650-000-2 from: 1 to: 461

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226 HisThrGlnProThrProGlyProSerThrAlaProSerThrSerPhe 242
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745 ....GGCTGGGCTCGACACCAAGGCG.....GGCCGCGCG 778
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242 uLeuProMetIlyProSerProPrrAlaGluGlySerThrIlyAspPhe 259
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272 ..GlyLeuIleuIleIleGlyValValAsnGlyValIleMetThrGln 287
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287 llyIlyIlySerProLeuIlyCysLeuGlnArgGluAlaIlyValProHisLeu 304
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917 CT 918  
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seq\_name: /cgn2\_6/ptodata/2/lae/6B\_COMB.pep:us-08-477-347-3

seq\_documentation\_block:

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Sequence 3, Application US/08477347
Patent No. 623246
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
TITLE OF INVENTION: TNF LIGANDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,347
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/115,685
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-347-3

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alignment\_scores:

Quality: 355.00 Length: 334  
Ratio: 1.994 Gaps: 13  
Percent Similarity: 53.293 Percent Identity: 29.940

alignment\_block:

US-09-006-352-1 x US-08-477-347-3 ..

Align seg 1/1 to: US-08-477-347-3 from: 1 to: 461

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374 CCGCTCTTCCGCGCAGCGTGT.....TTCGCTTG 405
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155 uThrSerAspValAlaCysIlyscysProCysAlaProGlyThrPheSerant 172
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556 GGCCGCGCCCTCATATGTCAGAGGCTCTCTCCATGACACCCCTGTGAC 605
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779 CTTTGACAGCTGAGCTGCTGCGGGGCTCAGGAGACCTCTGCGGGCGCAG 828
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seq_documentation_block:
; Sequence 1, Application US/08243010
; Patent No. 5639597
; GENERAL INFORMATION:
; APPLICANT: Lafleur, Leander
; APPLICANT: Zeitlmeisel, Gerd
; APPLICANT: Oquendo, Patricia
; TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
; TITLE OF INVENTION: Production and Use Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,010
; FILING DATE: 13-MAY-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/798,564
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: DE P 40 37 837.3
; FILING DATE: 28-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 02481-1132-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 486 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-243-010-1
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Ratio: 2.613 Gaps: 7
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101 GlnAlaArgAlaCysHisAlaThrHisAsnArgAlaCysArgTyrTh 117
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seq\_documentation\_block:

; Sequence 5, Application US/08974022

; Patent No. 6015938

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; APPLICANT: Lacey, David L.

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? APPLICANT: Calzone, Frank J.
? APPLICANT: Chang, Ming-Shi
? TITLE OF INVENTION: OSTEOPROTEGERIN
? NUMBER OF SEQUENCES: 53
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Amgen Inc.
? STREET: 1840 Dehavenland Drive
? CITY: Thousand Oaks
? STATE: California
? COUNTRY: USA
? ZIP: 91320-1789
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/974,022
? FILING DATE: 12-DEC-1995
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/577,788
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Winter, Robert B.
? REFERENCE/DOCKET NUMBER: A-378
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1355 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 94..1296
? US-08-974-022-5

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; Sequence 3, Application: US/08385229
; Patent No. 5605690
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Cindy A.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Method of Treating TNF-Dependent
; TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,229
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,236
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wright, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 587-0606
; INFORMATION FOR SEQ ID NO: 3:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1557 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: TNFR/Fc Fusion Protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1557
; NAME/KEY: mat_peptide
; LOCATION: 1..1554
; US-08-385-229-3

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alignment_scores:
Quality: 355.50 Length: 283
Ratio: 2.222 Gaps: 10
Percent Similarity: 56.537 Percent Identity: 32.155

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Align seq 1/1 to: US-08-385-229-3 from: 1 to: 1557

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1 seq documentation block:
2 Sequence 1, Application US/08385229
3 Patient No. 5605690
4
5 GENERAL INFORMATION:
6 APPLICANT: Jacobs, Cindy A.
7 APPLICANT: Smith, Craig A.
8 TITLE OF INVENTION: Method of Treating TNF-Dependent
9 TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
10 NUMBER OF SEQUENCES: 5
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Immunex Corporation
13 STREET: 51 University Street
14 CITY: Seattle
15 STATE: Washington
16 COUNTRY: U.S.A.
17 ZIP: 98101
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: PatentIn Release #1.0, Version #1.25
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/385,229
26 FILING DATE:
27 CLASSIFICATION: 435
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US/07/946,236
30 FILING DATE:
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Wight, Christopher L.
33 REGISTRATION NUMBER: 31,680
34 REFERENCE/DOCKET NUMBER: 2503
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (206) 587-0430
37 TELEFAX: (206) 587-0606
38 INFORMATION FOR SEQ ID NO: 1:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 1641 base pairs
41 TYPE: nucleic acid
42 STRANDEDNESS: single
43 TOPOLOGY: linear
44 MOLECULE TYPE: cDNA
45 HYPOTHETICAL: NO
46 ANTI-SENSE: NO
47 ORIGINAL SOURCE:
48 ORGANISM: Homo sapiens
49 CELL TYPE: Fibroblast
50

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1 CELL LINE: WI-26 VA4
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3 IMMEDIATE SOURCE:
4 LIBRARY: WI-26 VA4
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6 CLONE: Clone 1
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8 FEATURE:
9 NAME/KEY: CDS
10 LOCATION: 88..1473
11
12 FEATURE:
13 NAME/KEY: mat.peptide
14 LOCATION: 154..1470
15
16 FEATURE:
17 NAME/KEY: sig.peptide
18 LOCATION: 88..153
19
20 US-08-385-229-1

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alignment_scores:
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  Ratio: 2.234         Gaps: 11
  Percent Similarity: 54.110  Percent Identity: 31.5077

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[illegible]



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206 oGlyAlaGluLucysgluArgAlaValIleAspPheValAlaPheGlnA 223
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720 AGGGGAGTACACTTACCCAGCCA.....GTGTCACACGAT 757
223 spIleSerIleLys.ArgLeuGlnArg.....LeuGlnAlaLeuGln 237
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seq_documentation_block:
; Sequence 1, Application US/08650000
; Patent No. 5945397
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,000
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,453
; FILING DATE:
; APPLICATION NUMBER: US/08/038,765
; FILING DATE:
; APPLICATION NUMBER: US 403,241
; FILING DATE: 05-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 405,370
; FILING DATE: 11-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 421,417
; FILING DATE: 13-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,635
; FILING DATE: 10-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wight, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2501-D
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1641 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Fibroblast
; CELL LINE: WI-26 V44
; IMMEDIATE SOURCE:
; LIBRARY: WI-26 V44
; CLONE: 1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..1473
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 154..1470
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 88..153
; PUBLICATION INFORMATION:
; AUTHORS: Smith, Craig A.
; AUTHORS: Davis, Terri
; AUTHORS: Anderson, Dirk
; AUTHORS: Solam, Lisabeth
; AUTHORS: Beckmann, M. P.
; AUTHORS: Jerzy, Rita
; AUTHORS: Dower, Steven K.
; AUTHORS: Cosman, David
; AUTHORS: Goodwin, Raymond G.
; TITLE: A Receptor for Tumor Necrosis Factor Defines
; TITLE: an Unusual Family of Cellular and Viral Proteins
; JOURNAL: Science
; VOLUME: 248
; PAGES: 1019-1023
; DATE: 25-MAY-1990
; US-08-650-000-1

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      Ratio: 2.234      Gaps: 11
Percent Similarity: 54.110      Percent Identity: 31.507

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US-09-006-352-2 x US-08-650-000-1 ..

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seq_name: /cgn2_6/ptodata/2/lina/backfiles1.seq;5395760-1

seq_documentation_block:
Patent No. 5395760
Applicant: SMITH, CRAIG A.;GOODWIN, RAYMOND G.;BECKMANN, M. PATRICIA
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
:p-RECEPTORS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
APPLICATION NUMBER: 403,241
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[illegible]

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808 TTCCTGCTCCCAATGGGCGCCAGCCGCC.....C 836
254 InLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAspGly 270
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; Sequence 2, Application US/08477347
; Patent No. 6232446
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,347
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/115,685
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 90..1472
; US-08-477-347-2
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Ratio: 2.234 Gaps: 11
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62 sArgArgAspSerProThrThrCysGlyProCysProProlArgHisTyrt 79
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340 CCCAGCTGTGGAGTGGTCCCGAGTCTTGAGCTGTGGTCCCGCTCCGCTG 389
96 GlyLuarGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAl 112
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440 CTGCACCTGCGAGCGCGGCTGTGACTCGCGCTGACGACAGCAGAGGGGT 489
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490 GCGGCTGTGGCGCGCGCTGGCGAGTGGCGGCTTGGCGTGGCGG 539
140 AlaProGlyThrProSerGlnAsnThrGlnCysGlnProCysProProgl 156
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237 uAlaProGluGlyTrpGlyProThrProArgAlaGlyArgAlaAlaLeuG 254
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Mon Nov 5 08:22:41 2001

US-09-006-352-2.in1

Page 10

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; Sequence 11, Application US/08762308
; Patent No. 5925548
; GENERAL INFORMATION:
; APPLICANT: Beutler, Bruce A.
; TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,308
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,593
; FILING DATE: 05-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSD-335--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 418-3000
; TELEFAX: 474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3796 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-762-308-11

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634 ACAAGTGAAGTCTGTGCGCCGAGTCCCACTAGTGCATGCCATCCAG 683
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seq_documentation_block:
; Sequence 3, Application US/08650000
; Patent No. 5945397
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
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; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
; RECEPTORS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/523,635
; FILING DATE: 10-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 421,417
; FILING DATE: 13-OCT-1989
; APPLICATION NUMBER: 405,370
; FILING DATE: 11-SEP-1989
; APPLICATION NUMBER: 403,241
; FILING DATE: 05-SEP-1989
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5395760-3

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  Quality: 332.50      Length: 273
  Ratio: 2.173         Gaps: 9
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   ::::: |||||:::|||||:::|||||:::|||||:::|||||:::
208 CAGATGCTGCTGTAATGCTCTGCTGCGCAATATGTGAACAATCTTCTG 257
   ::::: |||||:::|||||:::|||||:::|||||:::|||||:::
62 sArgArgAspSerProThrPheCysGlyProCysProProArgHisTyrT 79
   ::::: |||||:::|||||:::|||||:::|||||:::|||||:::
258 CAACAAGACCTCGACACCGTGTGCTGCGACGTGACGACCAAGCATGTATA 307
   ::::: |||||:::|||||:::|||||:::|||||:::|||||:::
79 hArgInPheTrpAspTyrLeuGluArgCysArgTyrCysAsnValLeuGys 95
   ::::: |||||:::|||||:::|||||:::|||||:::|||||:::
308 CCCAGCTGTGGAACACGATTCGTACATCTTTGAGCTGCGATCTTCCCTGT 357
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96 GlyGluArgGluGluGlnAlaArgAlaCysHisSalThrHisAsnArgAl 112
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112 acysArgCysArgThrGlyPhePhe.....AlaHisAlaGlyP 125
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139 lLeaAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCysProPr 155
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508 GCCAGGTTCAGAGCCCAATGAAATGCTGATGCAAGGCGCTGCGCC 557
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816 TACAAGGCTGCGATCTCTCTCTTCCATTTGGTGTGATGTGAGCAT 865
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seq_documentation_block:
; Sequence 12, Application US/08266080B
; Patent No. 5606031
; GENERAL INFORMATION:
; APPLICANT: Jack Lile
; APPLICANT: Tadabiko Kohno
; APPLICANT: Duane Bonam
; APPLICANT: Mary S. Rosendahl
; TITLE OF INVENTION: Production of Biologically Active
; TITLE OF INVENTION: Recombinant Neurotrophic Protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/266,080B
; FILING DATE: 27-JUNE-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,122
; FILING DATE: 09-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/087,912
; FILING DATE: 06-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/680,681
; FILING DATE: 04-APRIL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/594,126
; FILING DATE: 09-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/547,750
; FILING DATE: 02-JULY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/505,441
; FILING DATE: 06-APRIL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: SYNE200C5

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TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 793-3333  
 TELEFAX: (303) 793-3433  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 691 nucleotides  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-266-080B-12

alignment\_scores:  
 Quality: 324.00 Length: 184  
 Ratio: 2.945 Gaps: 4  
 Percent Similarity: 59.783 Percent Identity: 34.239

alignment\_block:

US-09-006-352-2 x US-08-266-080B-12 ..

Align seg 1/1 to: US-08-266-080B-12 from: 1 to: 691

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46 .....
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118 GlyPheHehAlaHisAlaGly.....PheCysLeuGlu 128
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145 eArgLsnThrGlnCysGlnProCysProGlyThrPheSerAlaSer 161
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 seq\_documentation\_block:

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Sequence 12, Application PC/TUS9505423
GENERAL INFORMATION:
APPLICANT: Jack Lile
APPLICANT: Tagahiko Kohno
APPLICANT: Duane Bonam
APPLICANT: Mary S. Rosendahl
TITLE OF INVENTION: Production of Biologically Active
TITLE OF INVENTION: Recombinant Neurotrophic Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05423
FILING DATE:
Prior Application DATA:
APPLICATION NUMBER: 08/266,090
FILING DATE: 27-JUNE-1994
Prior Application DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
Prior Application DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
Prior Application DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
Prior Application DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
Prior Application DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
Prior Application DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05423-12
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alignment\_scores:  
 Quality: 324.00 Length: 184  
 Ratio: 2.945 Gaps: 4  
 Percent Similarity: 59.783 Percent Identity: 34.239

alignment\_block:

US-09-006-352-2 x PCT-US95-05423-12 ..

Align seg 1/1 to: PCT-US95-05423-12 from: 1 to: 691

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30 ValAlaGluThrProThrTyProTPrArgAspAlaGluThrGlyGlu.. 45
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151 GTGCATTACACCTAGCTCCG.....GAACGGGTTCTAC 188
46 ..... ArgLeuValCysAlaG 51
189 CTGCGCGGCTCAGAGAACTACTATGACCAGACAGCTCAGATGTCTGCACGA 238
51 lncysProProGlyThrPheValGlnArgProCysArgArgAspSerPro 67
239 AGTCGTGCGCGGCGCCACACATGCMAAGTCTTCTGTACCAGACACTCGGAC 288
68 ThrThrCysGlyProCysProProArgHisTyrThrGlnPheTyrAspTyr 84
289 ACCGTGTGTGACTCCTGTGAGAGACACACATACACCCAGCTGTGAACTG 338
84 rLeuGlnArgCysArgTyrCysAsnValLeuCysGlyGlnArgGlnGln 101
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101 lvalAlaArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThr 117
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128 uHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProS 145
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162 SerSerSerSerGlnGlnCysGlnProHisArgAsnCysThrAlaLeuGln 178
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639 C.....ATCCCTGGGAATGCAGCAGGATGCAGTGCACAGT 676
195 er 195
677 CC 678
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2001, 12:36:51 ; Search time 17.3 Seconds  
(without alignments)  
1320.946 Million cell updates/sec

Title: US-09-006-352-2

Perfect score: 1634

Sequence: 1 MRALEGPGLSLCLVLALPA.....RVARRPGLERSVREFLPVH 300

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	351.5	20.5	461	1 A35356	tumor necrosis fac
2	333.5	20.4	459	2 148854	gene murine tumor
3	332.5	20.3	474	2 B38634	tumor necrosis fac
4	315	19.3	435	2 154182	tumor necrosis fac
5	262.5	16.1	349	2 D72175	g2r protein - vari
6	262.5	16.1	349	2 D36858	gene G4R protein -
7	262	16.0	348	2 T26623	hypothetical prote
8	236.5	14.5	325	2 B43692	T2 protein - rabbl
9	226	13.8	277	2 137552	OX40 homolog - hum
10	215	13.2	326	1 GQVZML	T2 protein - myom
11	214	13.1	271	2 S12783	OX40 antigen precu
12	211	12.9	277	2 A60771	B-cell activation
13	203	12.4	305	2 A46476	B cell-associated
14	198.5	12.1	272	2 148700	gene ox40 protein
15	186.5	11.4	595	2 A42086	CD30 antigen precu
16	185	11.3	256	2 B32393	T-cell antigen 4-1
17	176	10.8	416	1 JN0006	nerve growth facto
18	175.5	10.7	427	1 GQHNUN	nerve growth facto
19	174	10.6	255	2 138426	lymphocyte activat
20	170	10.4	425	1 A26431	nerve growth facto
21	159.5	9.8	260	1 A46517	CD27 antigen precu
22	155.5	9.5	327	2 A46484	apoptosis-mediatin
23	148.5	9.1	1574	2 T13954	MEGF protein - ra
24	148	9.1	250	1 A49053	CD27 antigen precu
25	147.5	9.0	5376	2 T42215	zonadhesin - mouse
26	145	8.9	335	2 A40036	apoptosis-mediatin
27	144	8.8	324	2 JC2395	Fas antigen precur
28	143.5	8.8	1289	2 T43251	furin (PC 3.4.21.7
29	143	8.8	1620	2 T27283	hypothetical prote

## ALIGNMENTS

RESULT 1

A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
C:Species: Homo sapiens (man)  
C>Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 08-Dec-2000  
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990  
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular A:Reference number: A35356; MUID:90260639  
A:Accession: A35356  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SMI>  
A:Cross-references: GB:M32115; NID:q189185; PIDN:AAA59929.1; PID:q189186  
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc A:Reference number: A36475; MUID:91045991  
A:Accession: A36475  
A>Status: preliminary  
A:Molecule type: mRNA  
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A:Cross-references: GB:M55994; GB:M38549; NID:q339757; PIDN:AAA36755.1; PID:q339758  
R:Demblic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellul A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
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A:Molecule type: protein  
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A:Note: sequence extracted from NCBI backbone (NCBI:63368, NCBI:P:q3371)  
R:Hehlart, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons A:Reference number: A36007; MUID:90349572  
A:Accession: A36007  
A>Status: preliminary  
A:Molecule type: mRNA  
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A:Cross-references: GB:M35857; NID:q339751; PIDN:AAA61262.1; PID:q339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990  
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor A:Reference number: A23666; MUID:91056048  
A:Accession: A23666  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOB>

FAS soluble protei  
tumor necrosis fac  
notch3 protein - h  
membrane glycoprot  
serine proteinase  
laminin alpha 5 ch  
laminin gamma 2 ch  
laminin gamma 5 fac  
protein-tyrosine k  
adhesive ligand ep  
laminin alpha-2 ch  
tumor necrosis fac  
hypothetical prote  
laminin gamma-1 ch  
notch 3 protein -  
tumor necrosis fac

R:Engelmann, H.; Novick, D.; Wallach, D.  
 J. Biol. Chem. 265, 1531-1536, 1990  
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
 A:Reference number: A35010; MUID:90110215  
 A:Accession: B35010  
 A>Status: Preliminary  
 A:Molecule type: protein  
 A:Residues: 27-31 <ENG>  
 R:Kuhmert, P.; Kemper, O.; Wallach, D.  
 Gene 150, 381-386, 1994  
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of  
 A:Reference number: I38094; MUID:9511934  
 A:Accession: I38094  
 A>Status: Preliminary; translated from GB/EMBL/DBJ  
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 A:Gene: GDB:TNFR2  
 A:Cross-references: GDB:125914; OMIM:191191  
 A:Map position: 1p36.2-1p36.2  
 A:Note: the list of introns is incomplete  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
 F:40-76/Domain: NGF receptor repeat homology <NG1>  
 F:78-119/Domain: NGF receptor repeat homology <NG2>  
 F:120-162/Domain: NGF receptor repeat homology <NG3>  
 F:164-201/Domain: NGF receptor repeat homology <NG4>  
 F:262-279/Domain: transmembrane #status predicted <TMN>  
 F:280-461/Domain: intracellular #status predicted <INT>  
 F:111.193/Binding site: carbohydrate (Asn) (covalent) #status predicted

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 DB 61 QHAAVFCTKTSIDTVCDSCEDSTYTQLMNMMPECLSCGSKSDQVETQACTREONRICTC 120  
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 QY 230 QRLQALAEAE-----GWCPTPRA---GRAALQKRLRLTELGLAQDQALLVRLQAL 280  
 DB 228 QPPEPSTASTSTFLPMGSPRAEGSTGDFALPVGLIVGTAL-----GLLIIGVNCV 282  
 QY 281 ---RVAMP-GLERSYVERFLP 298  
 DB 283 IMTVKKKKPCLCGRKAVPHLP 304

RESULT 2  
 148854  
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 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
 C:Accession: I48854  
 R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
 Mamm. Genome 5, 726-727, 1994

A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
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 A:Molecule type: mRNA  
 A:Residues: 1-459 <RES>  
 A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 20.4%; Score 333.5; DB 2; Length 459;  
 Best Local Similarity 29.7%; Pred. No. 1e-17;  
 Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;  
 QY 46 RLVCACCPGTFVQPCRRDSPPTGCPPRHYTOFWNYLERCRVCNVLCGEREEARAC 105  
 DB 37 QMCCACCPGQVYKHKCNKTSPTVCADCEASMYTQVWNOFRTCLSCSSCSTDQVETRAC 96  
 QY 106 HATHNRACRCRTGFE---AHAGF---FLEHASCPGAGVIAPTPSQNTQOCPCPGTF 158  
 DB 97 TKQNRVACACGAGRYCALKTHSGRCQCRKLSKCGFGFVASSRABPNGLKACAPGTF 156  
 QY 159 SASSSSPQCOPPHRNCATLGLALNVPGSSSHDTLCT---SCTGPPLSRVVGAECERAC 214  
 DB 157 SDTTSSTVDCRPHRICSTILA---IPGNASTAVCAPESPRLSAIPRLTYVSGPPEPSSQ 212  
 QY 215 VIDFVAFODISIKRLQRLQALAEAPGEGPTP---RGRRAALQKRLRLTELGLAQD 269  
 DB 213 PLD---QEPGSGQPRSLITLSL-----GSTPIIDSTMGISLIGLIVGTSL----- 257  
 QY 270 GALLVRLQAL---RVAMPGLERSYVERFLP 298  
 DB 258 GLMLGLVNCFLIVQKKRPSCLQDRQAVPHVP 290

RESULT 3  
 B38634  
 tumor necrosis factor receptor type 2 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
 C:Accession: B38634; A40254; S54816  
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto  
 A:Reference number: A38634; MUID:91187885  
 A:Accession: B38634  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <LEN>  
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
 R:Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J  
 Mol. Cell. Biol. 11, 3020-3026, 1991  
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f  
 A:Reference number: A40254; MUID:91246168  
 A:Accession: A40254  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <GEO>  
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
 R:Kismonopis, M.; Fellous, R.; Feldmann, M.; Chennaïjovsky, Y.  
 submitted to the EMBL Data Library May 1995  
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor  
 A:Reference number: S54816  
 A:Accession: S54816  
 A>Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-22 <NIS>  
 A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA50618.1; PID:g809044  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Keywords: cytokine receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
 F:40-77/Domain: NGF receptor repeat homology <NG1>  
 F:79-120/Domain: NGF receptor repeat homology

F:166-203/Domain: NGF receptor repeat homology <MG4>

Query Match 20.3%; Score 332.5; DB 2; Length 474;

Best Local Similarity 29.7%; Pred. No. 1.2e-17;

Matches 81; Conservative 44; Mismatches 109; Indels 39; Gaps 9;

QY 46 RLVCACCPGPTVQRPQRDSPTTCGPPRRHYTOFWNYLERCRCYNVLCGEREEBARAC 105  
::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||  
DB 52 QMCAACPGPGYVKHKCNKTSPTVCADCEASMTYQWNGFRITLSCSSSCOTTQVEIRAC 111  
QY 106 HATHNACRCRGFF----AHAGF---CLEHASCPCGAGVIATGTSQNTQCPCTPCTF 158  
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||  
DB 112 TQOONVVCACEGRCYCALKTHSSGRCQKRLSKCGPGFGVASSRAPNGVNLCAACAPGT 171  
QY 159 SASSSSECCOPHRNCTALGLNLVPGSSSHDTCT----SCGFPLSTRVPGAECGERA 214  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 172 SDTSTDYCRPRICSIILA---IPGNASTDVAACAPESPTLSAIRPLLYVSOPEPTRSO 227  
QY 215 VIDPVAQDLSIKRLQLQLALEAPGCGPTP-----RAGRAALQLKRRRLTELLGAOD 269  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 228 PLD---GEGPSGQTPSILITSL-----GSTPIEGSTKGISLPLGLIVGTSL----- 272  
QY 270 GALLVRLQAL-----RVANMPGLERSVRRERFLP 298  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 273 GLMLGLVNCILVQRKKRPSCLQADAKVPHVP 305

#### RESULT 4

154182 tumor necrosis factor receptor 2-related protein - human

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000

C:Accession: I54182

R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Bergh, H.; Marynen, P.

Genomics 16, 214-218, 1993

A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen

A:Reference number: I54182; MUID:93252381

A:Accession: I54182

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-435 <RES>

A:Cross-references: GB:I04270; NID:9339761; PIDN:AAA36757.1; PID:9339762

C:Genetics:

A:Gene: GDB:LTBR

A:Cross-references: GDB:1230195; OMIM:600979

A:Map position: 12p13.3-12p13.1

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 19.3%; Score 315; DB 2; Length 435;

Best Local Similarity 31.8%; Pred. No. 2.3e-16;

Matches 89; Conservative 29; Mismatches 120; Indels 42; Gaps 12;

QY 3 ALEGPGLSLCLVLAIPALLPVAVGAETPTV-----PWRDA-----ETGERLYCAQC 52  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 6 ATGAPGLAMPVLVGLFGLLAASQPAV---PPYASENQCRCQKEKYEYEPQHRICCSRC 62  
QY 53 PRCPTVQRCRDRSPTTCGPPRRHYTOFWNYL---ERCRCYNVLCGEREEBARACHATH 109  
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||  
DB 63 PRCPTVSAACSRIRDIYVCAICAEISYNEHNNJLTICQLCPRCPPVWG--LEETAPCTSKR 120  
QY 110 NRACRCRTGFEAHAGFCLF--H---ASCPCGA-GVIAPGTPSQNTQCPCTPCTPCTSS 162  
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||  
DB 121 KTCRCRQPGKFC-AANALETCTHCELLSDCPGTEAEIKDEYGVGNHNCVCKRGHONT 179  
QY 163 SSSSECCOPHRNCTALGLNLVPGSSSHDTCTCTGFPPLSTRVPGAECGERAVIDVAQ 222  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 180 SPARQCPHRCRNOGIVLEAPGTAOSDTTCKNPLE-PLPEKMSGTMLMLAVLLPLAFL 238  
QY 223 DIS-----IKRLQLQLALEAPGCGPTPRAG 249  
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 239 LLATVESCIMKSHPSLCRLGSLK--RRPGGPGPNVAG 276

#### RESULT 5

D72175 G2R protein - variola minor virus (strain Garcia-1966)

C:Species: variola minor virus

C>Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 20-Jun-2000

C:Accession: D72175

R:Shchelkunov, S.N.; Tolmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lo

submitted to GenBank, March 1998

A:Description: Analysis of the complete coding sequence of DNA of alastrim variola mi

A:Reference number: A72150

A:Accession: D72175

A:Molecule type: DNA

A>Status: preliminary

A:Residues: 1-349 <SHC>

A:Cross-references: GB:I16780; NID:9583055; PIDN:CA854798.1; PID:95830759

A:Experimental source: strain Garcia-1966

C:Genetics:

A:Gene: G2R

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 16.1%; Score 262.5; DB 2; Length 349;

Best Local Similarity 30.0%; Pred. No. 1.6e-12;

Matches 62; Conservative 29; Mismatches 103; Indels 13; Gaps 3;

QY 9 LSLCLVLAIPALLPVAVGAETPTVPRDAETGERLYCACCPGTFVQRCRDRSPT 68  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 10 LFLSCITINGRDAAPYTPPENGCKDTEY-----KRHNLCCLSCPPTGYSLRCLDSKTN 63  
QY 69 TCGPCPPRRHYTOFWNYLERCRCYNVLCGEREEBARACHATHNRCRRTGFF-----AH 122  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 64 QCRPGSGFTSRNNHLPALSCNGRCSNQVETRSCNTHNNHNCESPCYCYCLKGSSG 123  
QY 123 AGCLCHASCPCGAGVIATGTSQNTQCPCTPCTSSSSSBQCPHRNCTALGLALN 182  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 124 CKACVSKTKGICIGYV-SGHTSVGDVLCSPCGCTYSYVSSDCKEPPVNNFTNYIDVE 182  
QY 183 VPSSSHDTLCTCTGFPPLSTRVGA 209  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB 183 ITLYPVNDTSCTRTTGTGSESLITSE 209

#### RESULT 6

D36858 gene: G2R protein - variola virus

N:Alternate names: B28R protein (COP)

C:Species: variola virus

C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Mar-2001

C:Accession: D36858; S46888; S32385; S35987

R:Blinov, V.M.

submitted to GenBank, November 1992

A:Reference number: A36859

A:Accession: D36858

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 <BLT>

A:Cross-references: GB:X69198; NID:9456758; PIDN:CA449137.1; PID:9457087

A:Experimental source: strain India-1967, ssp. major, isolate Ind3

R:Kol'yhalov, A.A.; Blinov, V.M.; Gylorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; F

submitted to the EMBL Data Library, April 1992

A:Description: Nucleotide sequence analysis of the region of Variola virus XHOI F O H

A:Reference number: S46868

A:Accession: S46888

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 <KOL>

A:Cross-references: EMBL:X67117; NID:9516428; PIDN:CA447540.1; PID:9516449

A:Experimental source: strain India-1967, isolate Ind3

R:Shchelkunov, S.N.; Blinov, V.M.; Sandakchiev, U.S.

FEBS Lett. 319, 80-83, 1993

A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protect

A:Reference number: S32385; MUID:93202281  
 A:Accession: S32385  
 A:Molecule type: DNA  
 A:Residues: 31-168 <SHC>  
 A:Cross-references: EMBL:X69198  
 A:Experimental source: strain India-1967, sep. major  
 C:Gene: G4R  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
 F:32-66/Domain: NGF receptor repeat homology <NGF>  
 F:68-109/Domain: NGF receptor repeat homology <NG2>  
 F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 16.1%; Score 262.5; DB 2; Length 349;  
 Best Local Similarity 30.0%; Pred. No. 1.6e-12;  
 Matches 62; Conservative 29; Mismatches 103; Indels 13; Gaps 3;  
 QY 9 LSLICLVIALPALLPVAVGVAEPTPYPMRDAETGERLVCAOCPPGTFFVQRCRRDSPT 68  
 DB 10 LFLSCIIINGRDAAPYPPNCKDKTEY-----KRNNLCCLSCPPGTASRLDSKNT 63  
 QY 69 TCGPCPRHYTOFWNYLERCYCNVLCGEREEBARACHATHNRCRRTGEF-----AH 122  
 DB 64 QCPFGSGGTFRNNHLPACISGRCNSNOVETRSCNTTHNRICEGSPGYCILKSSG 123  
 QY 123 AGFLEHASCPPGAGVIAPTGPSONTQCPCPPGTFSASSSSSECCQPHNRCTALGLALN 182  
 DB 124 CKACVSQTKGIGYGV--SGHTSVGDVLCSPGFGTYSHTVSSADKCPVNNTFNYIDVE 182  
 QY 183 VPSSSHDTICTSCGTGFPPLSTRVPGAE 209  
 DB 183 ITLYPVNDTSCRTTGTGLESILTSE 209

RESULT 7  
 T28623  
 hypothetical protein G2R - variola major virus  
 C:Species: variola major virus  
 C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
 C:Accession: T28623  
 R:Mass: 366,748,751,1993  
 R:Mass: 366,748,751,1993  
 A:Title: Potential virulence determinants in terminal regions of variola smallpox virus  
 A:Reference number: Z20488; MUID:94088747  
 A:Accession: T28623  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-348 <MMS>  
 A:Cross-references: EMBL:L22579; NID:9623595; PIDN:AAA60933.1; PID:9439102  
 A:Experimental source: strain Bangladesh 1975  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 16.0%; Score 262; DB 2; Length 348;  
 Best Local Similarity 30.8%; Pred. No. 1.7e-12;  
 Matches 64; Conservative 28; Mismatches 100; Indels 16; Gaps 4;  
 QY 9 LSLICLVIALPALLPVAVGVAEPTPYPMRDAETGERLVCAOCPPGTFFVQRCRRDSP 67  
 DB 10 LFLSCIIINGRDAAPYPPNCKDKTEY-----KRNNLCCLSCPPGTASRLDSKNT 61  
 QY 68 TTGCPGPRHYTOFWNYLERCYCNVLCGEREEBARACHATHNRCRRTGEF-----A 121  
 DB 62 TCGPCPRHYTOFWNYLERCYCNVLCGEREEBARACHATHNRCRRTGEF-----A 121  
 QY 122 HAFCLEHASCPPGAGVIAPTGPSONTQCPCPPGTFSASSSSSECCQPHNRCTALGLAL 181  
 DB 122 GCACVSQTKGIGYGV--SGHTSVGDVLCSPGFGTYSHTVSSADKCPVNNTFNYIDV 180  
 QY 182 NVGSSSHDTICTSCGTGFPPLSTRVPGAE 209  
 DB 181 EITLYPVNDTSCRTTGTGLESILTSE 208

RESULT 8  
 B43692  
 T2 protein - rabbit fibroma virus  
 C:Species: rabbit fibroma virus, Shope fibroma virus  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: B43692  
 R:Upton, C.; Delange, A.M.; McFadden, G.  
 A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomer  
 A:Reference number: A43692; MUID:87321103  
 A:Accession: B43692  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-325 <UPT>  
 A:Cross-references: GB:M17433  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
 F:64-105/Domain: NGF receptor repeat homology <NG2>  
 F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 14.5%; Score 236.5; DB 2; Length 325;  
 Best Local Similarity 29.9%; Pred. No. 1.3e-10;  
 Matches 58; Conservative 25; Mismatches 94; Indels 17; Gaps 4;  
 QY 11 LSLICLVIALPALLPVAVGVAEPTPYPMRDAETGERLVCAOCPPGTFFVQRCRRDSPT 70  
 DB 8 LVCVVVYGDVYSSNCKGSHDY-----EKDGLCCASCHPFGYASRLCGPSNTVC 61  
 QY 71 GCPGPRHYTOFWNYLERCYCNVLCGEREEBARACHATHNRCRRTGEF-----HAG 124  
 DB 62 SPEDGTFFASINHAPACVSCGPGTGHLSQPCDRTHDRNCSTGNVCLIKGQNCGR 121  
 QY 125 FCLEHASCPPGAGVIAPTGPSONTQCPCPPGTFSASSSSSECCQPHNRCTALGLALN 184  
 DB 122 ICAPQTKCPAGYGV--SGHTRAGDTLCKCPHPTYSLSLPTSCGTSEFYSVGNL--- 177  
 QY 185 GSSSHDTICTSCGTG 198  
 DB 178 -YPVNETSCRTTAG 190

RESULT 9  
 I37552  
 OX40 homolog - human  
 C:Species: Homo sapiens (man)  
 C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
 C:Accession: I37552  
 R:Latza, U.; Durkop, H.; Schlittger, S.; Ringeling, J.; Eltelbach, F.; Hummel, M.; Fo  
 Eur. J. Immunol. 24, 677-683, 1994  
 A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignmen  
 A:Reference number: I37552; MUID:94170844  
 A:Accession: I37552  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-277 <RES>  
 A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:9472958  
 C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 13.8%; Score 226; DB 2; Length 277;  
 Best Local Similarity 27.0%; Pred. No. 6.6e-10;  
 Matches 80; Conservative 25; Mismatches 117; Indels 74; Gaps 12;  
 QY 6 GPELSLICLVIALPALLPVAVGVAEPTPYPMRDAETGERLVCAOCPPGTFFVQRCRRD 65  
 DB 11 GPVALLLGLIGISTVTHCY-----GDTYPSNR-----CCHECRGMMSRCSRS 59  
 QY 66 SPTTCGCPPRHYTOFWNY--LERCYCNVLCGEREEBARACHATHNRCRRTGEFFAHA 123  
 DB 60 QNTVCRPCGPGYGVNDVSSKPKPCTWNLRSQ--SERKOLCTATQDVCRCRAG----- 112



OY 163 SSSECCOPHRNCATLGLALNVPGSSSHDPLC 193  
 B cell-associated surface molecule CD40, long splice form - mouse  
 C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
 C:Accession: A46476; A46515  
 R:Torres, R.M.; Clark, E.A.  
 J:Immunol. 148, 620-626, 1992  
 A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine  
 A:Reference number: A46476; MUID:92105763  
 A:Accession: A46476  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-305 <TOR>

RESULT 13

A:Cross-references: GB:M83312; NID:91553058  
 A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)  
 A:Note: this translation is not annotated in Genbank entry M83CD40, release 113.0  
 R:Imamul, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,  
 J:Immunol. 149, 3921-3926, 1992  
 A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
 A:Reference number: A46515; MUID:93094586  
 A:Accession: A46515  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-287, 'LV' <GRI>  
 A:Cross-references: GB:M83312; NID:91553058; PIDN:AAB08705.1; PID:91553059; GB:M94126; N  
 A:Experimental source: BALB/c, liver  
 A:Note: sequence extracted from NCBI backbone (NCBI:P:120357)  
 C:Comment: For an alternative splice form, see PIR:A46476.  
 C:Superfamily: CD27 antigen; NGF receptor repeat homology  
 C:Keywords: alternative splicing; transmembrane protein  
 F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match

Best Local Similarity 12.4%; Score 203; DB 2; Length 305;  
 Matches 47; Conservative 19; Mismatches 77; Indels 8; Gaps 3;

OY 49 CAOCPPGTFVORPCRDSPPTGCPPRHYTOFWNYLERC--RYCNVLCGEREEARAC 105  
 B 38 CDLCOPGSRILSHCTALEKTQCHPCDSGFSQWNRREIRCHQHRHCEPNOGLRVKKGST- 96  
 OY 106 HATNRACRCRTGFEFA--HAGFCLHASCPRGAGVIAPRPSONTGOCPPPTGFSASS 162  
 B 97 -AESDTVCTCKEGCHTSKDCACAHTRPCIFGFMKAEHTDTYCHPCPGVFGFSNOS 155  
 OY 163 SSSECCOPHRNCATLGLALNVPGSSSHDPLC 193  
 B 156 SLFECYFPMWSCDEKLVLELOKCTOTNYVIC 186

RESULT 14

gene OX40 protein - mouse  
 N:Alternate names: OX40 antigen  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000  
 C:Accession: 148700; 148334; S34377  
 R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;  
 J:Immunol. 151, 5261-5271, 1993  
 A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell int  
 A:Reference number: 148700; MUID:94044750  
 A:Accession: 148700  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-272 <RES>

A:Cross-references: EMBL:Z21674; NID:9312827; PIDN:CA479772.1; PID:9312828  
 R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.  
 E:U. Immunol. 25, 926-930, 1995  
 A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX  
 A:Reference number: 148334; MUID:95255413  
 A:Accession: 148334  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'G', '16-272 <RE2>  
 A:Cross-references: EMBL:X85214; NID:9732818; PIDN:CA459476.1; PID:9732819  
 C:Gene: OX40  
 A:Insertions: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1  
 C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match

Best Local Similarity 12.1%; Score 198.5; DB 2; Length 272;  
 Matches 57; Conservative 17; Mismatches 71; Indels 43; Gaps 8;

OY 15 VLALPALLVPVAVRGVAFETPYWRDAETGERLVCAQCPGTFVGRPCRDSPPTGCP 74  
 B 11 LLLALTLGVATRLNLCVKHTP-----SGHK-CRECPGIGMVRCDHTRDTLCPCHE 64  
 OY 75 PRHYTOFWNY--LEGRYCNVLCGEREEARACAHATNRACRCRTGFPFAHAGFCLHASC 132  
 B 65 TGFYNEAVVYDTCQCTCNHRSQ--SELKONCTPTQDTVCRCR----- 106  
 OY 133 PRGAGVIAGT-PSQNT-----OCOPCPGTFPSASSSECCOPHRNCATLGLALNVPG 185  
 B 107 -----PGTQPRDSCYKGLVCYVCPGHH--SPGNNAQCKWTKTCTLSGQTHRA 156  
 OY 186 SSSECCOPHRNCATLGLALNVPGSSSHDPLC 193  
 B 157 SDSLDVNC 164

RESULT 15

CD30 antigen precursor - human  
 N:Alternate names: Ki-1 antigen; nerve growth factor receptor family member CD30  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jul-2000  
 C:Accession: A42086  
 R:Durkop, H.; Latza, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein, H.  
 Cell 68, 421-427, 1992  
 A:Title: Molecular cloning and expression of a new member of the nerve growth factor  
 A:Reference number: A42086; MUID:92154659  
 A:Accession: A42086  
 A:Molecule type: mRNA  
 A:Residues: 1-595 <DGR>  
 A:Cross-references: GB:M83554; NID:9180095; PIDN:AAA51947.1; PID:9180096  
 A:Experimental source: HUT-102 cell line  
 A:Note: sequence extracted from NCBI backbone (NCBIN:82088, NCBI:P:82090)  
 C:Genetics:  
 A:Gene: GDB:CD30; DIS166E  
 A:Cross-references: GDB:131547; OMIM:153243  
 A:Map position: 1p36-1p36  
 C:Superfamily: NGF receptor repeat homology  
 C:Keywords: glycoprotein; growth factor receptor; transmembrane protein  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-383/Domain: extracellular #status predicted <EXT>  
 F:384-407/Domain: transmembrane #status predicted <TM>  
 F:408-595/Domain: intracellular #status predicted <INT>  
 F:101/276/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match

Best Local Similarity 11.4%; Score 186.5; DB 2; Length 595;  
 Matches 59; Conservative 23; Mismatches 82; Indels 33; Gaps 11;

OY 15 VLALPALLVPVAVRGVAFETPYWRDAETGERLVCAQCPGTFVGRPCRDSPPTG 70  
 B 11 LLLALTLGVATRLNLCVKHTP-----SGHK-CRECPGIGMVRCDHTRDTLCPCHE 64

```

Db      10 LFLGALRAFPQDRPPEDTCHGNPSHY---DKAVRRCYRCPMGLFPTQQCPQ-RPTDC 65
QY      71 -GPCPPRHYYTOFWNNYLERCRYCNVLCGERE-EEARACHATHNRACRORTGFFAHAGF--- 125
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      66 RKQCEPDYTL---DEADRCTAC-VTCSRDDLVEKTPCAMNSSRVCCECRPGMFCSTSAVNS 121
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      126 ---CLEHASCPPGAGVIAPIGTPSONTQQCPCPGTFSSASSSSSECCQ-----PHRNCT 175
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      122 CARCFHSHVCPAGMIYKFPGTAKNTVCEPASBGV-SPACASPENCKEPSSGTIPQAKPT 180
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      176 ALGLALNVPSSSHDTL 192
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 PVS-----PATSSASTM 192
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Search completed: October 31, 2001, 12:39:33  
 Job time: 162 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 31, 2001, 12:39:12 ; Search time 10.26 Seconds

(without alignments)  
1001.622 Million cell updates/sec

Title: US-09-006-352-2

Perfect score: 1634

Sequence: 1 MRALEGPGLSLCLVLAIPA.....RVARMPGLERSVEREPLPVH 300

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	353.5	21.6	461	1 TNR2_HUMAN	P20333 homo sapien
2	332.5	20.3	474	1 TNR2_MOUSE	P25119 mus musculu
3	315	19.3	435	1 TNRC_HUMAN	P36941 homo sapien
4	277	17.0	415	1 TNRC_MOUSE	P50284 mus musculu
5	262.5	16.1	349	1 VC22_VARV	P34015 varitola vir
6	236.5	14.5	325	1 VT2_SEVKA	P25943 shope fibro
7	226	13.8	277	1 OX40_HUMAN	P43489 homo sapien
8	215	13.2	326	1 VT2_MXYVL	P29825 myxoma viru
9	214	13.1	271	1 OX40_RAT	P15725 rattus norv
10	211	12.9	277	1 CD40_HUMAN	P25942 homo sapien
11	203	12.4	289	1 CD40_MOUSE	P27512 mus musculu
12	202	12.4	269	1 CD40_BOVIN	P28203 bos taurus
13	198.5	12.1	272	1 OX40_MOUSE	P47741 mus musculu
14	186.5	11.4	256	1 CD30_HUMAN	P28908 homo sapien
15	185	11.3	255	1 41BB_MOUSE	P20334 mus musculu
16	176	10.8	416	1 NGFR_CHICK	P18519 gallus gall
17	175.5	10.7	427	1 NGFR_HUMAN	P08138 homo sapien
18	174	10.6	255	1 41BB_HUMAN	P07011 homo sapien
19	170	10.4	425	1 NGFR_RAT	P07174 rattus norv
20	163	10.0	332	1 FASN_PIG	O77336 sus scrofa
21	160.5	9.8	471	1 TNRI_BOVIN	O19131 bos taurus
22	155.5	9.5	260	1 CD27_HUMAN	P25446 mus musculu
23	155.5	9.5	327	1 FASN_MOUSE	P51867 bos taurus
24	155	9.1	323	1 FASN_BOVIN	P41272 mus musculu
25	148	9.1	250	1 CD27_MOUSE	P25445 homo sapien
26	145	8.9	335	1 FASN_HUMAN	P25445 homo sapien
27	144	8.8	324	1 FASN_RAT	O63199 rattus norv
28	137.5	8.4	454	1 TNRI_MOUSE	P25118 mus musculu
29	129.5	7.9	1877	1 PKC5_MOUSE	O04592 mus musculu
30	128.5	7.9	417	1 WS11_HUMAN	O93038 h wsl-1 pro
31	128.5	7.9	3635	1 LMA5_MOUSE	O61001 mus musculu
32	127	7.8	1192	1 LMG2_MOUSE	O61092 mus musculu
33	125.5	7.7	461	1 TNRI_RAT	P22934 rattus norv

34	125.5	7.7	1255	1 ERB2_HUMAN	P04626 homo sapien
35	124.5	7.6	1696	1 PKC5_BRACL	O9n115 brachiocto
36	124.5	7.6	1713	1 TNR2_HUMAN	O16787 mus sapien
37	124.5	7.6	3106	1 LMA2_MOUSE	O60675 mus musculu
38	123.5	7.6	455	1 TNRI_HUMAN	P19438 homo sapien
39	123.5	7.6	2813	1 VWF_CANFA	O28395 canis famli
40	123	7.5	2569	1 LMA3_MOUSE	O61789 mus musculu
41	120	7.3	1609	1 LMG1_HUMAN	P11047 homo sapien
42	119.5	7.3	2318	1 NTC3_MOUSE	O61982 mus musculu
43	119.5	7.3	461	1 TNRI_PIG	P50555 sus scrofa
44	119.5	7.3	3084	1 LMA1_MOUSE	P19137 mus musculu
45	118.5	7.3	1680	1 FUR2_DROME	P30432 drosophila

#### ALIGNMENTS

RESULT: 1  
ID TNR2\_HUMAN STANDARD: PRT; 461 AA.  
AC P20333;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR  
GN TNFRSF1B OR TNFR2 OR TNFR). (P80) (TNF-R2) (P75) (CD120b) (ETANERCEPT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE-90260639; PubMed-2160731;  
RX MEDLINE-90260639; PubMed-2160731;  
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
RA Power S.K., Cosman D., Goodwin R.G.,  
RT "A receptor for tumor necrosis factor defines an unusual family of  
RT cellular and viral proteins.";  
RL Science 248:1019-1023(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-91045991; PubMed-2172983;  
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.,  
RT "A second tumor necrosis factor receptor gene product can shed a  
RT naturally occurring tumor necrosis factor inhibitor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-96299745; PubMed-8661109;  
RA Bellinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
RA Lepallier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,  
RA Brodeur G.M.,  
RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
RL Genomics 35:94-100(1996).  
RN [4]  
RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE-90349572; PubMed-2166946;  
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
RA Ringold G.M.,  
RT "Complementary DNA cloning of a receptor for tumor necrosis factor  
RT and demonstration of a shed form of the receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
RN [5]  
RP SEQUENCE OF 27-31.  
RX MEDLINE-90110215; PubMed-2153136;  
RA Engelmann H., Novick D., Wallach D.,  
RT "Two tumor necrosis factor-binding proteins purified from human  
RT tumor necrosis factor receptors.";  
RL J. Biol. Chem. 265:1531-1536(1990).  
RN [6]  
RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.

RA MEDLINE-91056048; PubMed=2173696;  
 RA Loetscher H., Schlaeager E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
 RA Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two  
 RT distinct tumor necrosis factor receptors from HL60 cells.";  
 RT J. Biol. Chem. 265:20131-20138(1990).  
 [7]  
 RP CHARACTERIZATION:  
 RX MEDLINE-93016040; PubMed=1328224;  
 RA Dennis D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
 RA Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 RT Characterization of ligand binding, internalization, and receptor  
 RT phosphorylation.";  
 RT J. Biol. Chem. 267:21172-21178(1992).  
 RL (8)  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.  
 RX MEDLINE-99221490; PubMed=10206649;  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of  
 RT human TRAF2.";  
 RT Nature 398:533-538(1999).  
 RL Nature 398:533-538(1999).  
 CC - FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND  
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC - PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW  
 CC LEVEL ON THREONINE RESIDUES.  
 CC - PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND  
 CC WEETH-AYERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID  
 CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING  
 CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO  
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.  
 CC - SIMILARITY: CONTAINS A IA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC - DATABASE: NAME=PROV; NOTE=CD guide CD120b entry,  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm"  
 CC - DATABASE: NAME=Enbrel; NOTE=Clinical Information on Enbrel;  
 CC WWW="http://www.enbrelinfo.com/".  
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 CC  
 DR EMBL; M32315; AAA59929.1; -;  
 DR EMBL; M35857; AAC63362.1; -;  
 DR EMBL; U52165; AAC50622.1; JOINED.  
 DR EMBL; U52156; AAC50622.1; JOINED.  
 DR EMBL; U52157; AAC50622.1; JOINED.  
 DR EMBL; U52158; AAC50622.1; JOINED.  
 DR EMBL; U52159; AAC50622.1; JOINED.  
 DR EMBL; U52160; AAC50622.1; JOINED.  
 DR EMBL; U52161; AAC50622.1; JOINED.  
 DR EMBL; U52162; AAC50622.1; JOINED.  
 DR EMBL; U52163; AAC50622.1; JOINED.  
 DR EMBL; U52164; AAC50622.1; JOINED.  
 DR EMBL; M55994; AAA36755.1; JOINED.  
 DR PIR; A35356; A35356;  
 DR PIR; A36007; A36007;  
 DR PIR; A36475; A36475;  
 DR PIR; B35010; B35010;  
 DR PIR; A23666; A23666;  
 DR PIR; ICA9; 12-APR-99.  
 DR MIM; 191191; -;  
 DR InterPro; IPR001368; -;  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00650; TNFR\_NGFR\_2; 4.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
 RX Phosphorylation; Pharmaceutical; 3D-structure.  
 FT SIGNAL 1 22

FT CHAIN 23 461  
 FT DOMAIN 23 257  
 FT TRANSMEM 258 287  
 FT DOMAIN 288 461  
 FT DOMAIN 39 201  
 FT REPEAT 39 76  
 FT REPEAT 77 118  
 FT REPEAT 119 162  
 FT REPEAT 163 201  
 FT DISULFID 40 53  
 FT DISULFID 34 62  
 FT DISULFID 57 75  
 FT DISULFID 78 93  
 FT DISULFID 96 110  
 FT DISULFID 100 118  
 FT DISULFID 120 126  
 FT DISULFID 134 143  
 FT DISULFID 137 161  
 FT DISULFID 164 179  
 FT CARBOHYD 171 193  
 FT CARBOHYD 193 193  
 FT CONFLICT 141 141  
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 FT CONFLICT 196 196  
 FT CONFLICT 363 363  
 SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;  
 Query Match 21.6%; Score 353.5; DB 1; Length 461;  
 Best Local Similarity 29.8%; Pred No 8.2e-21;  
 Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;  
 QY 8 GLSLICLVLPALPPVAVRGVAEPPTTYWRDAE-----RLVCAQCPG 55  
 DB 13 GLELMAAALPLA-----QVAFPIAP-----EGSCRLREYDDQAMKCSGSPG 60  
 QY 56 TVVQPCRDSPPTGCGPCPRPHHTQFWNTLRCRYCNVLGGEREEARACHATNPRAC 115  
 DB 61 QHAKVFCTKSDTVDCSDCEDSTYTQLMNVPECLSGSCSSSDVQTOACTREONITCY 120  
 QY 116 RTGFFAHAG-----FCLHASCPPAGVIAPTPSQNTQOCPCPGTFSASSSSDQO 169  
 DB 121 RPYWCALSKQECRCRLCAPLRKCRPGVAPGTETSDVVCRCAPGTFSNTSSDLCR 180  
 QY 170 PHNCTALGLALVWPSSSHDTLCTCTGPTLSTRVGAEECERAVIDVAFODISIKRL 229  
 DB 181 PQCICNVVA-----IPGNASRDVACTSTS--PTRSMAPGAVHLPEQV-----STRSQT 227  
 QY 230 QRLQALEAPE-----GNGPTPRA-----GRVALQTLRRRTFLGAQDGLVRLQL 280  
 DB 228 QPTPEPSTAPSTFLLPMGSPSPAESGTGDFALPVGLIYGTAL-----GLIIGVNCV 282  
 QY 281 ---RVARNP--GLERSVRERLP 298  
 DB 283 IMTVKKKPLCLQREAKVPLP 304  
 RESULT 2  
 TNFR\_MOUSE STANDARD: PRT: 474 AA.  
 ID TNFR\_MOUSE  
 AC P25119; P97893;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).  
 GN TNFRSF1B OR TNFR2 OR TNFR-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NOBI\_Taxid=10090;  
 RN [1]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE-9187885; PubMed=1849278;  
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,

RA Wong G.H., Chen E.Y., Goeddel D.V.;  
 RT "Cloning and expression of cDNAs for two distinct murine tumor  
 RT necrosis factor receptors demonstrate one receptor is species  
 RT specific.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerzy R., Brannan C.I.,  
 RA Copeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor.";  
 RL Mol. Cell. Biol. 11:3020-3026(1991).  
 RN [3]  
 RP SEQUENCE OF 1-26 FROM N.A.  
 RC STRAIN=MOD;  
 RA Jacob C.O., Liu J.;  
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE=Liver;  
 RA Kisseneigh M., Fellowes R., Feldmann M., Chernaiovsky Y.;  
 RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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 DR EMBL: M60469; AAA39752.1; -  
 DR EMBL: M59378; AAA40463.1; -  
 DR EMBL: U39488; AAA85021.1; -  
 DR EMBL: X87128; CAA60618.1; -  
 DR PIR: B38634; B38634.  
 DR HSP: P19438; I1NCF.  
 DR MGI: 1314883; Tnf1rflb.  
 DR InterPro: IPR001368; -  
 DR Pfam: PF00020; TNFR\_C6; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 474  
 FT DOMAIN 23 258 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT TRANSMEM 259 288 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 289 474 POTENTIAL.  
 FT DOMAIN 39 203 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 39 77 4 X TNFR-CYS.  
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 FT DISULFID 101 119 BY SIMILARITY.  
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 FT DISULFID 136 145 BY SIMILARITY.  
 FT DISULFID 139 163 BY SIMILARITY.  
 FT DISULFID 166 191 BY SIMILARITY.  
 FT CARBOHYD 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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Query Match

20.3%; Score 332.5; DB 1; Length 474;

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 Db 52 QMCCACKCPGGQYVKKHCKNTSDVYCADCEASMTQVWVNCRTCLSSSSCTTQVETIRAC 111  
 QY 106 HATNHRACRGRGFE---AHAGF---CLEHASCPCGAGVIAGTPDSONTQCPGPTGF 158  
 Db 112 TKQNVNVCACAGRYCALTKTHSSCRQMRLSKCGFGVVASRAAPNGVLCACAPGTF 171  
 QY 159 SASSSSSDCCPHRNTALGLAINVPGSSSHDLCT---SCTGPISTVYPAECERA 214  
 Db 172 SDPTSTVDCRPHRICSTLA---IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 227  
 QY 215 VDFVAFQDISIKRLQRLQALPAEPGSGPTP-----RAGRALQKLRRRLTELLGAQD 269  
 Db 228 PLD-----QERGSPQTSILSL-----GSTPIIBOSTKGIPLGLIVGVISL----- 272  
 QY 270 GALLVRLLOAL---RVARMPLGERSVREERFLP 298  
 Db 273 GLMLGLVNCILIVQRKKRPSCLQRDAPKVPHP 305  
 RESULT 3  
 ID TNRC\_HUMAN STANDARD; PRT; 435 AA.  
 AC P36941;  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR  
 DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).  
 GN LTBR OR TNFR OR TNFRSF3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93252381; PubMed=8486360;  
 RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;  
 RT "Construction and evaluation of a hncDNA library of human 12p  
 RT transcribed sequences derived from a somatic cell hybrid.";  
 RL Genomics 16:214-218(1993).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=94225209; PubMed=8171323;  
 RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,  
 RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;  
 RT "A lymphotoxin-beta-specific receptor.";  
 RL Science 264:707-710(1994).  
 CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
 CC IMMUNE DEVELOPMENT.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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 CC -----  
 DR EMBL: L04270; AAA36757.1; -  
 DR HSP: P25942; ICDF.  
 DR MIM: 600979; -  
 DR InterPro: IPR001368; -  
 DR Pfam: PF00020; TNFR\_C6; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.

KW Receptor; Transmembrane; Glycoprotein; Repeat; signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 435  
 FT DOMAIN 31 227  
 FT TRANSMEM 228 248  
 FT DOMAIN 249 435  
 FT DOMAIN 442 211  
 FT REPEAT 42 81  
 FT REPEAT 82 124  
 FT REPEAT 125 168  
 FT REPEAT 169 211  
 FT DISULFID 43 56  
 FT DISULFID 59 72  
 FT DISULFID 62 80  
 FT DISULFID 83 98  
 FT DISULFID 101 116  
 FT DISULFID 104 124  
 FT DISULFID 126 132  
 FT DISULFID 139 148  
 FT DISULFID 142 167  
 FT DISULFID 170 185  
 FT CARBOHYD 40 40  
 FT CARBOHYD 177 177  
 SQ SEQUENCE 435 AA; 46709 MW; 62462656022F56F CRC64;

Query Match 19.3%; Score 315; DB 1; Length 435;  
 Best Local Similarity 31.8%; Pred. No. 8.1e-18;  
 Matches 89; Conservative 29; Mismatches 120; Indels 42; Gaps 12;

OY 3 ALEPGSLCLVLAIPALLVPVAVGVAETPTV-----PWRDA-----ETGERTVCAQC 52  
 DB 6 ATAPAGLWGLVGLGLGLLAASQPAV---PYASENQCRDQEKRYEPQHHCISRC 62  
 OY 53 PPGYVNCPRGRDPTTCGPRPRHYQFNYL---ERCRCNVLGGEREERACATH 109  
 DB 63 PPGYVNAKCRIDYCATCAENSYENHNYLTICQLCRCDYVAG--LEELAPCTSKR 120  
 OY 110 NRACRCRTPFAHAGFCLF-H-----ASCPRGA-GVAPGTPSONTCQCPPTGSASS 162  
 DB 121 KTCRCOCGPMFC-AAMALECTHCLSDCPGTAEALKDEYGNKNNCVCKAGHFQNTS 179  
 OY 163 SSSQCPHNRCTALGLALNVGSSSHDTLCTGCTGFPPLSTRVGAEECERAVIDEVAFQ 222  
 DB 180 SPSARCQPHRCENQGVLEAAPGTAQSDTTKNLE-PLPEMGTMLMLAVLPIAFL 238  
 OY 223 DIS-----TKRLQRLQALEAPEGMGPPTPRAG 249  
 DB 239 LIAVFSCIMKSHPSLCKRLKGLSLK--RRPGEGPDPVAG 276

RESULT 4  
 TNRC MOUSE STANDARD; PRT; 415 AA.  
 ID TNRC MOUSE STANDARD; PRT; 415 AA.  
 AC P50284;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.  
 GN ITBR OR TNFR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX MEDLINE=6072804; PubMed=7594541;  
 RA FORCE W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,  
 RA Browning J.L., Ware C.F.;  
 RA "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,  
 and expression.";  
 RL J. Immunol. 155:5280-5286(1995).

RN [2]  
 RN SEQUENCE FROM N.A.  
 RA MEDLINE=9616385; PubMed=8586432;  
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,  
 RA Honjo T.  
 RA "The murine lymphotoxin-beta receptor cDNA: isolation by the signal  
 sequence trap and chromosomal mapping.";  
 RT Genomics 30:312-319(1995)  
 CC - FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
 CC - IMMUNE DEVELOPMENT.  
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC  
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 CC  
 CC EMBL; U29173; AAA68964.1; -  
 CC EMBL; L38423; AAB00846.1; -  
 CC EMBL; U30798; AAB1334.1; -  
 CC HSSP; P25942; ICDF.  
 DR MGD; MGI:104875; Ltbr.  
 DR InterPro; IPR001368; -  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR ProSite; PS00652; TNFR\_NGFR\_1; 2.  
 DR ProSite; PS00050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 415  
 FT DOMAIN 31 223  
 FT TRANSMEM 224 244  
 FT DOMAIN 245 415  
 FT DOMAIN 42 213  
 FT REPEAT 42 81  
 FT REPEAT 82 124  
 FT REPEAT 125 170  
 FT REPEAT 171 213  
 FT DISULFID 43 58  
 FT DISULFID 59 72  
 FT DISULFID 62 80  
 FT DISULFID 83 98  
 FT DISULFID 101 116  
 FT DISULFID 104 124  
 FT DISULFID 126 132  
 FT DISULFID 139 150  
 FT DISULFID 142 169  
 FT DISULFID 172 187  
 FT CARBOHYD 40 40  
 FT CARBOHYD 179 179  
 SQ SEQUENCE 415 AA; 44956 MW; 29B326A56AE661 CRC64;

Query Match 17.0%; Score 277; DB 1; Length 415;  
 Best Local Similarity 31.2%; Pred. No. 7.4e-15;  
 Matches 88; Conservative 29; Mismatches 105; Indels 60; Gaps 14;

OY 6 GP-----GLSLCLVLAIPALLVPVAVGVAETPTVPRDAETGERL---VCAQCPPTGTYQ 59  
 DB 15 GPLLIGISGL-LVASQPOLVPPRI-----ENQICWDQDEVEYEPHMDVCCSCPGEEYF 69  
 OY 60 PCRGRDPTTCGPRPRHYQFNYL---ERCRCNVLGGEREERACATHNRCR 116  
 DB 70 AVCSRSQDVTYCKTCPRHNSYNEHNMHLSTCOLRCPICVIG--FEVAPCTSRKAECRCQ 127  
 OY 117 TGFPAHAGFCL-----BHASCOPGAGVIA-PGTPSONT-----OCQCPPTGFSASS 163  
 DB 128 PGM-----SCVYIDNCCVHCBEERLVIQPGTEAEVTDIMTDVVCYCKPGHFNQNTSS 182  
 OY 164 SSSQCPHNRCTALGLALNVGSSSHDTLCTGCTGFPPLSTRVGAEECERAVIDEVAF-- 221

```
Db 183 PRACOPHTRCEIQLGVEAAGTSTSYDTC-----NPEPGAMILLAILSLVLELL 235
QY 222 -----ODISIKRLQRLIALEAPEGWG-----PTPRA 248
Db 236 FTTVLACAMWHRHPSLCRKLTCTLLK--RHPEGEESPPOCPAPRA 275

RESULT 5
VC22_VARY STANDARD: PRT: 349 AA.
ID VC22_VARY
AC P34015:
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE PROTEIN C22/B28 HOMOLOG.
GN G4R.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-INDIA-1967 / ISOLATE IND3;
RX MEDLINE-93202281; PubMed-8364129;
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms."
RL FEBS Lett. 319:80-83(1993).
CC -1- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X69198; CAA49137.1; -
DR EMBL: X67117; CAA47540.1; -
DR PIR: D36858; D36858.
DR PIR: S35987; S35987.
DR PIR: S46888; S46888.
DR HSSP: P19438; 1NCF.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_c6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR Repeat.
KW DOMAIN 31 108 2 X TNFR-CYS.
FT REPEAT 31 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
SQ SEQUENCE 349 AA; 38189 MW; D45040B5C6E780EF CRC64;

Query Match 16.1%; Score 262.5; DB 1; Length 349;
Best Local Similarity 30.0%; Pred. No. 8.6e-14;
Matches 62; Conservative 29; Mismatches 103; Indels 13; Gaps 3;
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Db 183 ITLYPVNDTSCRTTGTGTSSEIITSE 209

RESULT 6
VT2_SFVKA STANDARD: PRT: 325 AA.
ID VT2_SFVKA
AC P25943;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=10272;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91207415; PubMed-1850261;
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA McFadden G., Goodwin R.G.;
RT "T2 open reading frame from the Shope fibroma virus encodes a soluble
RT form of the TNF receptor."
RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -----
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL: M17433; -; NOT ANNOTATED_CDS.
DR EMBL: A23727; CAA01687.1; -
DR PIR: B43692; B43692.
DR HSSP: P19438; 1TNR.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_c6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT DOMAIN 27 186 4 X TNFR-CYS.
FT REPEAT 27 62 TNFR-CYS 1.
FT REPEAT 63 104 TNFR-CYS 2.
FT REPEAT 105 147 TNFR-CYS 3.
FT REPEAT 148 186 TNFR-CYS 4.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;

Query Match 14.5%; Score 236.5; DB 1; Length 325;
Best Local Similarity 29.9%; Pred. No. 8.8e-12;
Matches 58; Conservative 25; Mismatches 94; Indels 17; Gaps 4;
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Db 8 LVGVVYVVGDDVPPSSNQGKGGCHD-----EKDGLCAASCHPGRVYASRLCGPSGNTVC 61  
 QY 71 GPRPHHYQFMNXYLERCRYNCLGEEFEERARCAHTHRACRKTGFFA-----HAG 122  
 Db 62 SPEDGTFTASTNHAAPACVSCGPGCTGHLSSQCDTHDRVNCSTGYVCLLKQNCGR 121  
 QY 125 FCLHNASCPGAGVIAPTGPSONTQCPGPGTFFSASSSSSEQCPHRNCTALGLALNVP 184  
 Db 122 ICAPQTKCPGAGVY-SGHTRAGDFTLCEKPCPHYSDLSLPTERCSTFNYISVGNL--- 177  
 QY 185 GSSSHDPLCTSCG 198  
 Db 178 -YPVNETSCITTAG 190

RESULT	7
ID	OX40_HUMAN
AC	P34389; O13663;
DT	01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	OX40L RECEPTOR PRECURSOR (ACT5 ANTIGEN) (TRAX-TRAASCRIPTIIONALLY
GN	ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
NC	TRNRS4 OR TYGPI1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid	9606;
RA	SEQUENCE FROM N.A.
RA	MEDLINE:941170844; PubMed-7510240;
RA	Latza U., Duerkop H., Schnaltger S., Ringeling J., Ettebach F.,
RA	Hummel M., Fonatsch C., Stein H.;
RT	"type human OX40 homology: cDNA structure, expression and chromosomal
RT	assignment of the ACT5 antigen.";
RL	Eur. J. Immunol. 24:677-683(1994).
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE:95219871; PubMed-774935;
RX	Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA	Watson M.L., Seidm M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT	"Identification of OX40 ligand and preliminary characterization of
RT	its activities on OX40 receptor.";
RL	Circ. Shock 44:30-34(1994).
CC	-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC	-!- SIMILARITY LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-!- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE Cysteine-RICH REGION.
CC	-!- DATABASE: NAME=PROM; NOTE=CD guide CD134 entry?
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL: X75962; CAAS3576.1; "
DR	EMBL: S76792; AAB33944.1; ALT_INIT.
DR	HSP: P25942; ICDF.
DR	MTM: 600315; "
DR	InterPro: IPR001368; "
DR	Pfam: PF00020; TNFR_G6; 3.
DR	PROSITE: PS00652; TNFR_NGFR_1; 3.
DR	PROSITE: PS00050; TNFR_NGFR_2; 2.
KM	Receptor; T cell; Antigen; Glycoprotein; Transmembrane; Repeat;
FT	Signal.
FT	1 28
FT	CHAIN 29 277
FT	DOMAIN 29 214
	POTENTIAL.
	OX40L RECEPTOR.
	EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	215	235	POTENTIAL.
FT	DOMAIN	236	277	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	30	169	4 X TNFR-CYS.
FT	REPEAT	30	65	TNFR-CYS 1.
FT	REPEAT	66	107	TNFR-CYS 2.
FT	REPEAT	108	126	TNFR-CYS 3 (INCOMPLETE).
FT	REPEAT	127	167	TNFR-CYS 4.
FT	CARBOHYD	146	160	N-LINKED (GLCNAC. ) (POTENTIAL).
FT	CARBOHYD	160	160	N-LINKED (GLCNAC. ) (POTENTIAL).
FT	CARBOHYD	277 AA:	29340 MM:	49F1532594A1550BF CRC64:

Query Match	13.8%;	Score 226;	DB 1;	Length 277;
Best Local Similarity	27.0%;	Pred. No. 5e-11;		
Matches	80;	Conservative	25;	Mismatches 117;
			Indels	74;
			Gaps	12

[illegible]

RESULT	8			
ID	VT2_MYXVL			
AC	P29825;	STANDARD:	PRt:	326 AA.
CC	01-APR-1993 (Rel. 25, Created)			
CC	01-APR-1993 (Rel. 25, Last sequence update)			
CC	15-JUL-1999 (Rel. 38, Last annotation update)			
CC	TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).			
CC	12.			
CC	Myxoma virus (strain Lausanne).			
CC	Viruses: dsDNA viruses, no RNA stage: Poxviridae; Chordopoxvirinae;			
CC	Leportipoxvirus.			
CC	NCBI_TaxId=31530;			
CC	[1]			
CC	SEQUENCE FROM N.A.			
CC	MEDLINE=9135768; PubMed=1651597;			
CC	Upton C., Macen J.L., Schreiber M., McFadden G.;			
CC	Myxoma virus expresses a secreted protein with homology to the tumor			
CC	necrosis factor receptor gene family that contributes to viral			
CC	virulence.";			
CC	virolology 184:370-382(1991).			
CC	-1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO			
CC	REACH CELLULAR TARGET AND THEREBY DAMENING THE POTENTIAL			
CC	ANTIVIRAL EFFECTS OF THE CYTOKINE.			
CC	-1- SIMILARITY: CONTAINS A LA-NCP/TNF-R-TYPE CYSTEINE-RICH REGION.			
CC	-----			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
CC	EMBL; M95181; AAA46632.1; -			
CC	EMBL; A23729; CAA01688.1; -			

DR PIR: A40566; GOVZML.  
DR HSSP: P19438; 1TNR.  
DR InterPro: IP001368; .  
DR Pfam: PF00020; TNR\_C6; 2.  
DR PROSITE: PS00652; TNR\_NGFR\_1; 2.  
DR PROSITE: PS50050; TNR\_NGFR\_2; 2.  
DR Receptor: Glycoprotein; Repeat; Signal.  
KW SIGNAL.  
FT CHAIN 1 16  
FT DOMAIN 17 36  
FT REPEAT 27 62  
FT REPEAT 63 104  
FT REPEAT 105 147  
FT REPEAT 148 186  
FT CARBOHYD 66 66  
FT CARBOHYD 181 181  
FT CARBOHYD 205 205  
FT CARBOHYD 238 238  
SQ SEQUENCE 326 AA; 35208 MW; ABBF027E947292FF CRC64;

Query Match 13.2%; Score 215; DB 1; Length 326;  
Best Local Similarity 29.3%; Pred. No. 4.3e-10;

Matches 58; Conservative 22; Mismatches 96; Indels 22; Gaps 5;

QY 12 LCLVLAIPALP-----PVAVRGVAETPTYPWRDAETGERLVCACGPPGTFVORPCRDSS 66  
DB 4 LTLALLVAVACVGGAGPYGADRGKRGNDY-----EKDGLCTCTSCPPGSYARLGGPGS 57  
QY 67 PTTGCGPPRHHTYQFMNYYLERCRYCNVLCGEREEBARACHATNNRACRCRTGFFA----- 121  
DB 58 DTVCSCKNKEFTASTNHAFCVSCRGRCRGLHSESOSCDKTRDRCDDCSAGNYCLIKGQ 117  
QY 122 -HAGFLEHASCPGAGVIAPGPGSONTOGQPCPGPFSSSSSSSECCOPHRNCTALGLA 180  
DB 118 EGRICAPPTKPCAGYGV-SGHTRTGDVLCCTKCPRTTSDAVSSTCTTSSFNIVISEFN 176  
QY 181 LNVPGSSSHDTLCSTGCT 198  
DB 177 L-----YPVNDTSCCTTAG 190

RESULT 9  
OX40\_RAT  
ID OX40\_RAT STANDARD; PRT; 271 AA.  
AC P15725;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).  
GN TNFRSF4 OR TNFRP1L OR OX40.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=T-cell;  
RX MEDLINE=90214614; PubMed=2157591;  
RA Mallet S., Fossum S., Barclay A.N.;  
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T  
lymphocytes -- a molecule related to nerve growth factor receptor.";  
RL EMO J. 9:1063-1068(1990).  
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/SP34 CYTOKINE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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DR EMBL: X17037; CA34897.1; .  
DR PIR: S08036; S08036.  
DR PIR: S12783; S12783.  
DR HSSP: P25942; 1CDF.  
DR InterPro: IP001368; .  
DR Pfam: PF00020; TNR\_C6; 3.  
DR PROSITE: PS00652; TNR\_NGFR\_1; 3.  
DR PROSITE: PS50050; TNR\_NGFR\_2; 2.  
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
KW Signal.  
FT CHAIN 1 19  
FT DOMAIN 20 27  
FT DOMAIN 20 210  
FT TRANSMEM 211 235  
FT DOMAIN 236 271  
FT DOMAIN 25 164  
FT REPEAT 25 60  
FT REPEAT 61 102  
FT REPEAT 103 123  
FT REPEAT 124 164  
FT CARBOHYD 143 143  
SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 13.1%; Score 214; DB 1; Length 271;  
Best Local Similarity 30.1%; Pred. No. 4.3e-10;

Matches 58; Conservative 23; Mismatches 64; Indels 48; Gaps 9;

QY 10 SLCLVLAIPALPVPVAVRGVAETPTYPWRDAETGERLVCACGPPGTFVORPCRDSPPT 69  
DB 10 AFLDGLSLGVTKYNKVK-----DTYP-----SGHK-CCRECGPGMGMSRCDHTRDYV 58  
QY 70 CGCPGPPRHHTYQFMNYYLERCRYCNVLCGEREEBARACHATNNRACRCRTGFFAHAGFCL 127  
DB 59 CHDCEPGFYNEAVNYDCKCQCTOCNHRSG--SELKONCTPEIDYVCCR----- 105  
QY 128 EHNSCPGAGVIAPGT-PSONT-----OCQPCPGPFSSSSSSSECCOPHRNCTALGLA 180  
DB 106 -----PGTQPRDSSHKLGVDVPCPPGHF--SPGSNACKKPMWCTTSLGKQ 150  
QY 181 LNVPGSSSHDTLC 193  
DB 151 IRRPASNSIDTVC 163

RESULT 10  
CD40\_HUMAN  
ID CD40\_HUMAN STANDARD; PRT; 277 AA.  
AC P25942;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)  
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).  
GN TNFRSF5 OR CD40.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=89356608; PubMed=2475341;  
RX Stamenkovic I., Clark E.A., Seed B.;  
RT "A B-lymphocyte activation molecule related to the nerve growth  
factor receptor and induced by cytokines in carcinomas.";  
RL EMO J. 8:1403-1410(1989).  
CC [2]  
CC 3D-STRUCTURE MODELING OF 24-144.  
RP MEDLINE=97189462; PubMed=9037712;  
RA Bajorath J., Aruffo A.;

"Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40.";  
 Proteins 27:59-70(1997).  
 [3]  
 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
 MEDLINE=98266353; PubMed=9605317;  
 RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,  
 RA Zhang Z., Naismith J.H., Thomas D.;  
 RT "The role of polar interactions in the molecular recognition of CD40L  
 with its receptor CD40.";  
 RL Protein Sci. 7:1124-1135(1998).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME=PROX; NOTE=CD guide CD40 entry;  
 WWW="http://www.ncbi.nlm.nih.gov/prox/cd/cd40.htm"  
 -----  
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 -----  
 DR EMBL; X60592; CAA43045.1; -  
 DR PIR; S04460; S04460.  
 DR PDB; 1CDF; 01-APR-97.  
 DR MIM; 109535; -  
 DR InterPro; IPR001368; -  
 DR Pfam; PF00020; TNFR.cf.4.  
 DR PROSITE; PS00652; TNFR.NGFR.1; 1.  
 DR PROSITE; PS50050; TNFR.NGFR.2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;  
 3D-structure.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 277 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 194 215 POTENTIAL.  
 FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT DISULFID 26 37  
 FT DISULFID 38 51  
 FT DISULFID 41 59  
 FT DISULFID 62 77  
 FT DISULFID 83 103  
 FT DISULFID 105 119  
 FT DISULFID 111 116  
 FT DISULFID 125 143  
 FT DISULFID 153 153  
 FT CARBOHYD 180 180  
 FT SEQUENCE 277 AA; 30619 MW; BC8776EC2CA45680 CRC64;  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 Query Match 12.9%; Score 211; DB 1; Length 277;  
 Best Local Similarity 30.5%; Pred. No. 7.5e-10;  
 Matches 46; Conservative 21; Mismatches 76; Indels 8; Gaps 3;

DB 156 SAFKCHPWTSCETKDLVVOAGTKNTDYVC 186  
 RESULT 11  
 ID CD40\_MOUSE STANDARD; PRT; 289 AA.  
 AC P27512;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40).  
 GN TNFRSF5 OR CD40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RA [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92105763; PubMed=1370315;  
 RA Torres R.M., Clark E.A.;  
 RT "Differential increase of an alternatively polyadenylated mRNA  
 species of murine CD40 upon B lymphocyte activation.";  
 RL J. Immunol. 148:620-626(1992).  
 (2)  
 RP REVISIONS.  
 RC STRAIN-BALB/C;  
 RA Torres R.M.;  
 RN Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE=Liver;  
 RA MEDLINE=93094586; PubMed=1281194;  
 RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,  
 RA Howard M., Cockayne D.A.;  
 RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";  
 RL J. Immunol. 149:3921-3926(1992).  
 -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 CC EMBL; M8312; AAB08705.1; -  
 DR EMBL; M94126; AAA37404.1; -  
 DR EMBL; M94129; AAA37404.1; JOINED.  
 DR EMBL; M94128; AAA37404.1; JOINED.  
 DR EMBL; M94127; AAA37404.1; JOINED.  
 DR PIR; A46476; A46476.  
 DR HSSP; P25942; 1CDF.  
 DR MGD; MGI:88336; TNFRsf5.  
 DR InterPro; IPR001368; -  
 DR Pfam; PF00020; TNFR.cf.4.  
 DR PROSITE; PS00652; TNFR.NGFR.1; 1.  
 DR PROSITE; PS50050; TNFR.NGFR.2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;  
 3D-structure.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 289 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 216 289 POTENTIAL.  
 FT DOMAIN 225 289 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT CARBOHYD 153 153  
 FT SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).









Mon Nov 5 08:22:43 2001

us-09-006-352-2.rsp

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 31, 2001, 12:38:21 ; Search time 19.71 Seconds  
(without alignments)  
2013.775 Million cell updates/sec

Title: US-09-006-352-2  
Perfect score: 1634  
Sequence: 1 MRALEPGSLLCVLAIPA.....RVANMPGLSVREPLPVH 300

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_16:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1634	100.0	300	4 095407	095407 homo sapien
2	444	27.2	401	4 000300	000300 homo sapien
3	440.5	27.0	372	4 09UH94	09UH94 homo sapien
4	425.5	26.0	401	11 008727	008727 rattus norv
5	424.5	26.0	401	11 008712	008712 mus musculu
6	395	24.2	302	13 09PU50	09PU50 mus musculu
7	340.5	20.8	439	4 016042	016042 homo sapien
8	333.5	20.4	459	11 062327	062327 mus musculu
9	327	20.0	482	11 088734	088734 mus musculu
10	291.5	17.8	655	11 09EP05	09EP05 mus musculu
11	287	17.6	655	4 075509	075509 homo sapien
12	282.5	17.3	348	14 057277	057277 monkeypox v
13	280.5	17.2	348	14 057103	057103 monkeypox v
14	280.5	17.2	348	14 057108	057108 monkeypox v
15	276	16.9	349	14 057100	057100 monkeypox v
16	274	16.8	349	14 057291	057291 monkeypox v
17	274	16.8	349	14 057101	057101 monkeypox v
18	274	16.8	349	14 057102	057102 monkeypox v
19	273	16.7	349	14 057099	057099 monkeypox v

20	265	16.2	350	14 057116	057116 cowpox viru
21	264.5	16.2	355	14 085308	085308 cowpox viru
22	262.5	16.1	349	14 057110	057110 variola vir
23	262.5	16.1	349	14 057111	057111 variola vir
24	262.5	16.1	349	14 089118	089118 variola vir
25	262.5	16.1	349	14 089098	089098 variola vir
26	262	16.0	348	14 057112	057112 variola vir
27	262	16.0	348	14 085407	085407 variola vir
28	261.5	16.0	349	14 057284	057284 camelpox vi
29	261.5	16.0	349	14 057098	057098 camelpox vi
30	259.5	15.9	349	14 057305	057305 cowpox viru
31	259.5	15.9	360	14 057118	057118 cowpox viru
32	258.5	15.8	351	14 057117	057117 cowpox viru
33	258.5	15.8	351	14 073559	073559 cowpox viru
34	257.5	15.8	326	14 057120	057120 cowpox viru
35	257.5	15.8	349	14 057097	057097 camelpox vi
36	254.5	15.6	326	14 057122	057122 cowpox viru
37	254.5	15.6	349	14 057109	057109 variola vir
38	253.5	15.5	347	14 057115	057115 cowpox viru
39	251.5	15.4	347	14 057119	057119 cowpox viru
40	250.5	15.3	351	14 057121	057121 cowpox viru
41	249	15.2	283	6 09XS28	09XS28 cercopithe
42	246	15.1	283	4 092956	092956 homo sapien
43	246	15.1	283	4 09UM65	09UM65 homo sapien
44	245.5	15.0	350	14 057123	057123 cowpox viru
45	239	14.6	616	4 09Y606	09Y606 homo sapien

## ALIGNMENTS

RESULT 1  
095407 PRELIMINARY: PRT: 300 AA.  
AC 095407;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE DECOY RECEPTOR 3 (M68) (M68C) (M68B) (DJ583p15.1.1).  
GN DCR3 OR TR6 OR TNFRSF6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99087326; PubMed=9872321;  
RA Pitti R.W., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,  
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,  
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,  
RA Goddard A.D., Bortstein D., Ashkenazi A.;  
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and  
RT colon cancer.";  
RT Nature 396:699-703(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE-BLOOD;  
RA MEDLINE=99253915; PubMed=10318773;  
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;  
RT "A newly identified member of tumor necrosis factor receptor  
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";  
RT J. Biol. Chem. 274:13733-13736(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX TISSUE-PANCREAS;  
RA MEDLINE=20122600; PubMed=10655513;  
RA Bai C., Connolly B., Metzger M.L., Hilliard C.A., Liu X., Sandig V.,  
RA Soderman A., Galloway S.M., Liu O., Austin C.P., Caskey C.T.;  
RT "Overexpression of M68/DCR3 in human gastrointestinal tract tumors  
RT independent of gene amplification and its location in a four-gene  
RT cluster.";  
RT Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).  
RN [4]



```
QY 11 LCLVALPALPVPVAVGVAET--PTWRAETGERLYVCAOCPGPTVQRCRDSPT 68
DB 4 LLLCAL---VFLDISIKMTQETFPKPYLYHDEETSHQLLDCDKCPGTYLKQCTAKMKP 60
QY 69 TCGCPRRHYTOFWNVLNLCRCRYCNVLCGEREERARACHATHNACRCRTGFFAHAGCLE 128
DB 61 VCAPCPDHYTTSMTSDCLCYSPVCKLQYVCKCNTHNHNVCCKEGRYLEIEFCLK 120
QY 129 HASCPPGAVIAPGTPSOMTQOCPPGPTFSASSSSSEOCOPRNCALGALANVPGSSS 188
DB 121 HNSCPGFGVQAGTERKNTVCRCRCDGFFSNSTSSKAPCRKHTNCSVGLLLTQKGMAT 180
QY 189 HDLTCTSCGFLSTRVPAEE--CERAVIDF 218
DB 181 HDNI---CSGNSESTQKCGIDVTLCEAFRRF 209

RESULT 3
QY 09UHP4 PRELIMINARY: PRT: 372 AA.
AC 09UHP4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11)
RP SEQUENCE FROM N.A.
RA TISSUE=PLACENTA;
RC He 2.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Li Hsueh Pao 31:680-684(1999).
DR EMBL: AF134187; AAF20168.1; -.
DR HSSP: P25942; ICDF.
DR InterPro: IPR000488; -.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00500; TNFR_NGFR_2; 2.
DR SMART: SM00005; DEATH; 1.
FT NON_TER 1
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;
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Query Match 27.0%; Score 440.5; DB 4; Length 372;
Best Local Similarity 41.2%; Pred. No. 1e-31;
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QY 34 PTPWMDAETGERLYVCAOCPGPTVQRCRDSPTGCPRRHYTOFWNVLNLCRCRYCNV 93
DB 5 PLYLHDEETSHQLLDCDKCPGTYLKQCTAKMKTVCACPDHYTSDMTSDECLYCSGP 64
QY 94 LCGEREERARACHATHNACRCRTGFFAHAGCLEHASCPPGAGVIAPTGSPONTQOCPC 153
DB 65 VCKELQYVAGQECRHTNHNVCCKEGRYLEIEFCLKHRSRCPGFGVQAGPRENTVCCKRC 124
QY 154 PCTFSASSSSSEOCOPRNCALGALANVPGSSSHDTLCTSGTGPLSTRVPAEE--C 211
DB 125 PDGFFSNSTSSKAPCRKHTNCSVGLLLTQKGMATDNI---CSGNSESTQKCGIDVTL 181
QY 212 ERAVIDF 218
DB 182 EEAFRRF 188

RESULT 4
QY 008727 PRELIMINARY: PRT: 401 AA.
AC 008727;
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DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCTP)
GN TNFRSF11B OR OPG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 11)
RP SEQUENCE FROM N.A.
RA TISSUE=INTESTINE;
RC MEDLINE=97262071; PubMed=9108485;
RX Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";
RL Cell 89:309-319(1997).
CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
SIMILARITY).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: U94330; AAB53707.1; -.
DR HSSP: P25942; ICDF.
DR InterPro: IPR000488; -.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00500; TNFR_NGFR_2; 2.
DR SMART: SM00005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1
FT CHAIN 21
FT DOMAIN 22 401
FT REPEAT 23 201
FT REPEAT 23 63
FT REPEAT 64 106
FT REPEAT 107 143
FT REPEAT 144 201
FT REPEAT 201 365
FT DOMAIN 365 401
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 118 142
FT DISULFID 145 160
FT CARBOHYD 98 98
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
SQ SEQUENCE 401 AA; 46192 MW; FEC6A31FID4E573A CRC64;
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Query Match 26.0%; Score 425.5; DB 11; Length 401;
Best Local Similarity 39.5%; Pred. No. 2.5e-30;
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;
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QY 34 PTPWMDAETGERLYVCAOCPGPTVQRCRDSPTGCPRRHYTOFWNVLNLCRCRYCNV 93
DB 26 PLYLHDEETSHQLLDCDKCPGTYLKQCTAKMKTVCACPDHYTSDMTSDECLYCSGP 85
QY 94 LCGEREERARACHATHNACRCRTGFFAHAGCLEHASCPPGAGVIAPTGSPONTQOCPC 153
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DB 86 VCKELQTVKQECNRTNRYNRCCECEGRVLELEPCLKHRSCPGVLQAGTFRNTVCRC 145
OY 154 PGFTFSASSSSSEOCOPHRNCTALGLALNVPGSSHDLTCTGTFPLSTRVPAEE--C 211
DB 146 PGFTFSASSSSKAPCRKHTNCSLLILLOKGNATHDNV---CSGNREATONCGIDVTL 202
OY 212 ERAVIDFAFODISIKRLOQLAL 236
DB 203 EEAFFRAVPTKIIIPWLSVLDL 227

RESULT 5
O08712 PRELIMINARY: PRT: 401 AA.
AC 008712.070202:
DN 01-JUL-1997 (TREMblrel. 04, Created)
DN 01-JUL-1997 (TREMblrel. 04, last sequence update)
DN 01-MAR-2001 (TREMblrel. 16, last annotation update)
DE OSTEOPOTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF).
GN TNSRFL1B OR OPG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-KIDNEY;
RA MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Desore M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Day E., Bucay N., Renshaw-Geeg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RT Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-129/OLA, AND NIH SWISS.
RA MEDLINE=96382527; PubMed=9714633;
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA Higashio K.;
RA "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
RT gene and its expression in embryogenesis.";
RL Gene 215:339-343(1998).
CC - FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC - SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
CC - TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
CC PLACENTA. NOT DETECTED IN SPLEEN.
CC - DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
CC 15 TO DAY 17.
CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: U94331; AAB53708.1; -
DR EMBL: AB013868; BAA38260.1; -
DR EMBL: AB013903; BAA33368.1; -
DR EMBL: AB013893; BAA33368.1; JOINED.
DR EMBL: AB013900; BAA33368.1; JOINED.
DR EMBL: AB013901; BAA33368.1; JOINED.
DR EMBL: AB013902; BAA33368.1; JOINED.
DR HSSP: P25942; ICDF.
DR GSSP: MG1:109587; TnfRsf11b.
DR InterPro: IPR000488; -
DR InterPro: IPR001368; -
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DR Pfam; PF00020; TNFR_C6; 3.
DR ProDom; PD000771; -; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401 OSTEOPOTEGERIN.
FT DOMAIN 23 201 4 X TNFR-CYS.
FT REPEAT 23 63
FT REPEAT 64 106 TNFR-CYS 1.
FT REPEAT 107 163 TNFR-CYS 2.
FT REPEAT 144 201 TNFR-CYS 3.
FT REPEAT 201 365 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH SWISS).
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH SWISS).
SQ SEQUENCE 401 AA; 45923 MW; CAA6102DB312470 CRC64;

Query Match 26.0%; Score 424.5; DB 11; Length 401;
Best Local Similarity 39.0%; Pred. No. 3; 1e-30;
Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;

OY 34 PTVPMWDAETGERLVCAOCPPGTGVORPCRPDSPTTGGCPPRHYTQFWNYLERCRYCNV 93
DB 26 PKLYHYDPEPGEHQLDCDKAPGTYLKHQCTVRRKTLVCPDHSYTDSWHTSDDEVYCS 85
OY 94 LCGEREERARACHATNRRACRRTGFFAAGFCLHASCPPGAGVAPGTSPQNTQOCOPC 153
DB 86 VCKELQTVKQECNRTNRYNRCCECEGRVLELEPCLKHRSCPGSVVQACTPERRNTVCRC 145
OY 154 PGFTFSASSSSSEOCOPHRNCTALGLALNVPGSSHDLTCTGTFPLSTRVPAEE--C 211
DB 146 PGFTFSASSSSKAPCRKHTNCSLLILLOKGNATHDNV---CSGNREATONCGIDVTL 202
OY 212 ERAVIDFAFODISIKRLOQLAL 236
DB 203 EEAFFRAVPTKIIIPWLSVLDL 227

RESULT 6
O09PUSO PRELIMINARY: PRT: 302 AA.
AC O09PUSO:
DN 01-MAY-2000 (TREMblrel. 13, Created)
DN 01-MAY-2000 (TREMblrel. 13, last sequence update)
DN 01-MAR-2001 (TREMblrel. 16, last annotation update)
DE DECOY RECEPTOR.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protactinopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_Taxid=8038;
```





DB 157 SDTSTSDVCRPHRICSLIA-----IPGNASPDVACAPESPTLSAIPRTLYVSOPEPTRSQ 212  
 OY 215 VIDFVAFODISIKRLQLOALEAPEGWGPPTP-----RAGRAALQKLRRLTELLGAOD 269  
 DB 213 PLD-----QEPGSPQSPISLTSL-----GSTPIIPOSTKSGISLPIGLIVGTVSL----- 257  
 OY 270 GALVLRLOAL-----RVANMPLEERSVREERFLP 298  
 DB 258 GLMLGLVNCFLVQKRRKPSCLQDRAVPHVP 290

RESULT 9  
 O88734 PRELIMINARY: PRT: 482 AA.  
 AC O88734;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE P80 TNF-ALPHA RECEPTOR.  
 GN TNFR2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN 11)  
 RP SEQUENCE FROM N.A.  
 RA Huile B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;  
 RT "The Mouse Tumor Necrosis Factor Receptor Gene: Genomic Structure and  
 RT Characterization of the two Transcripts."  
 RL Genomics 0:0-0(0).  
 DR EMBL: Y14619; CAI74969.1; JOINED.  
 DR EMBL: Y14621; CAI74969.1; JOINED.  
 DR EMBL: Y14621; CAI74969.1; JOINED.  
 DR EMBL: Y14622; CAI74969.1; JOINED.  
 DR EMBL: Y14623; CAI74969.1; JOINED.  
 DR EMBL: Y14679; CAI74969.1; JOINED.  
 DR HSSP: p19438; INCE.  
 DR InterPro: IPR001368;  
 DR Pfam: PF00020; TNFR\_C6; 4.  
 DR ProDom: PD000771;  
 DR PROSITE: PS00652; TNFR\_LNGFR\_1; 2.  
 DR PROSITE: PS00650; TNFR\_LNGFR\_2; 3.  
 DR SMART: SM00208; TNFR; 1.  
 SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;

Query Match 20.0%; Score 327; DB 11; Length 482;  
 Best Local Similarity 29.3%; Pred. No. 2e-21;  
 Matches 82; Conservative 43; Mismatches 109; Indels 46; Gaps 10;  
 OY 46 RLVCACCPGPTVORPCRR-----DSPTTCGPCPPRHNYQFNWYLERGRCYNVLCGER 98  
 DB 52 QMCKACKCPGQYVHKHCNKTSDTVACADSDTVACADCEAMSYQVWNNORFTLCSSSSCSTD 111  
 OY 99 EEEARACNATHNARACRTGFP-----AHACF---CLEHASCPPGAVIAGTPSONTOCO 151  
 DB 112 QVETRACTCOORVACCEGRYCALKTHSGSCROCMRLSKGPGFVASSAPRGNVLCK 171  
 OY 152 PPPGFFSSSSSSBOCPHRCALAGLWVSSSHDTCT-----SCGFPPLSTVPG 207  
 DB 172 ACAPGFSOTSTSDVCRPHRICSLIA-----IPGNASPDVACAPESPTLSAIPRTLYVSO 227  
 OY 208 AECECAVYDFAVADISIKRLQLOALEAPEGWGPPTP-----RAGRAALQKLRRLTE 262  
 DB 228 PEPTSPQD-----QEPGSPQSPISLTSL-----GSTPIIPOSTKSGISLPIGLIVGTV 277  
 OY 263 ELGACDALLVRLQAL-----RVANMPLEERSVREERFLP 298  
 DB 278 SL-----GLMLGLVNCFLVQKRRKPSCLQDRAVPHVP 312

RESULT 10  
 Q9EPUS

ID Q9EPUS PRELIMINARY: PRT: 655 AA.  
 AC Q9EPUS;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE DR6  
 DE Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN 11)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=KIDNEY;  
 RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,  
 RA Minami M.;  
 RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6  
 RT (DR6)."  
 RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AF322069; AAC38115.1;  
 DR EMBL: AF322069; AAC38115.1;  
 SQ SEQUENCE 655 AA; 71909 MW; 1A97C1A32799E4FB CRC64;

Query Match 17.8%; Score 291.5; DB 11; Length 655;  
 Best Local Similarity 28.6%; Pred. No. 4.2e-18;  
 Matches 73; Conservative 37; Mismatches 130; Indels 15; Gaps 3;  
 OY 12 LCLVLAFLALLPVAVRGVATPTYPWRDAETGERLYCACCPGPTVORPCRRDPTTCG 71  
 DB 30 LLLIGFLSTIAOPEOKTSLPGTYRHVDRTGGVLTCDKCPAGTVSEHCTNMSLRVCS 89  
 OY 72 PCPPRHNYQFNWYLERGRCYNVLCGEREEARACHATHNARACRTGFPAAHAGFCLENAS 131  
 DB 90 SCPATFTFRHNGIERCHDCSQPCWPMIERLCALITDECCICPPGQMSNGTCAPIHV 149  
 OY 132 CPBGAVIAGTPSONTOCPCPPTGTSASSSECOCPHRCALAGLWVSSSHDTCT 191  
 DB 150 CPVGVVRRKKGITSDVSNVWKCAHFDCLQGLVLEVRKGTETDN 209  
 OY 192 ICTSGTGPPL---STRVGAEECECAVYDFAVADISIKRLQLOALEAPEGWGPPTPRA 248  
 DB 210 VC-----GRLFFSSSTNPSSGTGTFSPHEHSHDPSSTYE-----PGQMNSTDN 257  
 OY 249 GAAIQKLRRLTE 263  
 DB 258 STASVTRKVPGIEE 272

RESULT 11  
 O75509 PRELIMINARY: PRT: 655 AA.  
 ID O75509;  
 AC O75509;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE TNFR-RELATED DEATH RECEPTOR-6 (DJ181J13.1) (DR6 (TNFR-RELATED DEATH  
 DE RECEPTOR-6)).  
 DE DR6 OR DJ181J13.1.  
 GN Homo sapiens (Human).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN 11)  
 RP SEQUENCE FROM N.A.  
 RA Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Yu G.,  
 RA Vincenz C., Aggarwal B.B., Dixit V.M.;  
 RT Identification and functional characterization of DR6, a novel death  
 RT domain-containing TNF receptor.  
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
 RN 12)  
 RP SEQUENCE FROM N.A.  
 RA Parker A.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF068868; AAC34583.1;



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RN SPOUNCE FROM N.A.
RP STRAIN-ZAIRE-1970 (CONGO-8);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted Feb-1997 to the EMBL/GenBank/DBJ databases.
DR EMBL: U08842; AAB94367.1; -.
DR HSSP: p25942; ICDF.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_c6; 2.
DR ProDom: PD000771; -.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00500; TNFR_NGFR_2; 2.
DR SMART: SM00208; TNFR; 1.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;

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Query Match 17.2%; Score 280.5; DB 14; Length 348;  
 Best Local Similarity 30.4%; Pred. No. 2.2e-17;  
 Matches 63; Conservative 34; Mismatches 97; Indels 13; Gaps 3;

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OY 9 LSLCLVLPALPVPVAVGVATPTYPWRDAETGERLVCAOCPPTGVORPCRRDSPT 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 10 LFLSCIIINGRIDIAHPASNGKCKDNEYRSRN-----LCCLSCPPGTYYASRLCDSKNT 63
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 69 TCGPCPPRIHYTOFMNYLERCRYCNVLCGEREEARACAHATHNRCRCRTGFF-----AH 122
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 64 OCTPGSDPTFTSHNNHLOACLSCNGRCDNSNOVETRSCNTNHNRLCECSPGYCYLLKGSSG 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 123 AGFCLEHASCPPGAGVIAFGTPSQNTQCQPCPPGTFSASSSSSEOCOPHRNCTALGLAN 182
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 124 CRTCLSKTKGIGYGV-SGYTSDGVICSPCGGTYSHTVSSDCKCEPVTSNTFNVIDE 182
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 183 VPGSSSHDTLCTSCGTFPLSTRVPAE 209
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 183 INLYPNDSCTRTTTGLSISISTSE 209
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RESULT 15
ID 057100 PRELIMINARY; PRT; 349 AA.
AC 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID-10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NIGERIA-1971 (71-0082);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U87844; AAB94361.1; -.
DR HSSP: p25942; ICDF.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_c6; 2.
DR ProDom: PD000771; -.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00500; TNFR_NGFR_2; 2.
DR SMART: SM00208; TNFR; 1.
SQ SEQUENCE 349 AA; 38239 MW; DFC6280D478F2422 CRC64;

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Query Match 16.9%; Score 276; DB 14; Length 349;  
 Best Local Similarity 30.0%; Pred. No. 5.5e-17;  
 Matches 63; Conservative 34; Mismatches 95; Indels 18; Gaps 5;

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OY 9 LSLCLVLPALPVPVAVGVATPTYPWRDAETGERLVCAOCPPTGVORPCRRDSPT 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 10 LFLSCIIINGRIDIAHPASNGKCKDNEYRSRN-----LCCLSCPPGTYYASRLCDSKNT 63
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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OY 69 TCGPCPPRIHYTOFMNYLERCRYCNVLCGEREEARACAHATHNRCRCRTGFF-----AH 122
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 64 OCTPGSDPTFTSHNNHLOACLSCNGRCDNSNOVETRSCNTNHNRLCECSPGYCYLLKGASG 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 123 AGFCLEHASCPPGAGVIAFGTPSQNTQCQPCPPGTFSASSSSSEOCOP--HRNCTALGL 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 124 CSTCLSKTKGIGYGV-SGYTSDGVICSPCGGTYSHTVSSDCKCEPVTSNTFNVIDE 182
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 180 ALNVPSSSHDTLCTSCGTFPLSTRVPAE 209
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 183 EIML--YPNVDTSCTRTTTGLSISISTSE 210
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248 CAGTGGCCCCAGGACCTTTGTGAGGGCCGTGGCCGAGACAGCC 297  
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298 CAGAGGTGTGGCCGTGTCCACGCCGCACTACACAGCATCTGTGAACT 347  
84 yrlcugluarvcysargtyrcysasnvalleucysglygluaagluglu 100  
348 ACCTGGAGCGCTGCCCTACTACGCAACGTCCTCTCGGGGAGCGCTGAGAG 397  
101 glnalargalacysahisalaThrhisasnargalacysargysarph 117  
398 GAGGACAGGCGTTGCCACGCCACACACCGTCTCGCCGCTGGCCGAC 447  
117 rglphrphelalhisalaglyphrcysleugluhlsalasercysprop 134  
448 CGGCTCTTGGCGACGCTGGTTCTGTGGACGACGATCGTGTGCAC 497  
134 roglalaglyalllealaprogllythrproserglnasnthrglncys 150  
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548 CACGCGTCCCCAGCAACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCA 597  
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SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: DCTP/DTP/Gazdar  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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98 gglugluGlnAlaArgAlaCysNhsAlaThrhisAsnArgAlaCysArgC 115  
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454 CTGCTGAGGCGCTGAGAGCGCCGAGAGCGTGGGTCTCCAGCACCAAGGCG 503  
248 aglyArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeu 265



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VERSION BE878006.1 GI:10326782
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 679)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM9677 row: h column: 21
High quality sequence stop: 672.
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NciI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT 113 a 239 c 204 g 123 t
ORIGIN
alignment_scores:
Quality: 1020.00 Length: 192
Ratio: 5.312 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-006-352-2 x BE878006 ..
Align seg 1/1 to: BE878006 from: 1 to: 679
109 HisnsmaralacysargcysargThrglyphephealalHisalaglyph 125
|||||
12 CACACACGGCTGCTCGCTGCCACCGGCTTCTCGGCGACGCTGCTTT 61
125 ecysleugluh1slaserCysProProglYAlaGlYValleAlaProG 142
|||||
62 CTGCTTGAGCAGCAGTCGTCCACCTGGTGGCGGCGTGTATGCCCGG 111
```

```
142 lYthrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPhe 158
|||||
112 GCACCCCGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 161
159 SerAlaSerSerSerSerSerGlnCysGlnProCysProProGlyThrPhe 175
|||||
132 TCAGCAGCAGCTCCAGCTCAGAGCAGTGCAGAGCCGACCCGACGACGAC 211
175 rAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrL 192
|||||
212 GGCCCTGGGCGCTGGCCCTCAATGTGCTCCAGGCTCTTCTCCATGACACC 261
192 euCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAla 208
|||||
262 TGTGCACAGCTGACCTGCTTCCCTCCAGCAGGAGGTACAGAGAGCT 311
209 GlnGlnCysGlnArgAlaValIleAspPheValAlaPheGlnAspIleSe 225
|||||
312 GAGGAGTGTAGCGTGGCTCATCGACTTGTGTGCTTCCAGGACATCTGC 361
225 rIleYsArgLeuGlnArgLeuLeuGlnAlaLeuGlnAlaProGlyLys 242
|||||
362 CATCAAGAGCTGACGCGCTGCTGCTGACAGCCCTGAGGCGCGAGGCT 411
242 rpglyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArg 258
|||||
412 GGGCTCCACACCAAGGCGGCGCGCGCGCTTGCACCTGACCTGAGTGGT 461
259 ArgArgLeuThrGlnLeuLeuGlnAlaGlnAspGlyAlaLeuLeuValAr 275
|||||
462 CGGGGCTCAGCGAGCTCTGGGGCGCAGAGCGGGGCTGTGTGTGCG 511
275 gLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlnArgSerV 292
|||||
512 GCTGCTGACGCGCGCTGCCGCTGCCAGATGCCGCGCTGAGCGAGCG 561
292 aArgGluArgPheLeuProValHis 300
|||||
562 TCCGAGACGCTTCTCCCTGCGAC 587
seq_name: gb_est47:AM464298
seq_documentation_block:
LOCUS AM464298 554 bp mRNA EST 24-FEB-2000
DEFINITION BP230015A20G11 Soares normalized bovine placenta Bos taurus cDNA
clone BP230015A20G11 5', mRNA sequence.
ACCESSION AM464298
VERSION AM464298.1 GI:7034466
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 554)
AUTHORS Lewin,H.A., Soares,M.B., Rebeliz,M., Pardinas,J., Liu,L. and Larson
,J.H.
TITLES Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimml 9:
Cross_match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
```

PCR primers  
 FORWARD: TAAATACGACTCCTATAGG  
 BACKWARD: ATTTACCTCTCATAG  
 Insert Length: 534 Std Error: 0.00  
 Plate: BP230015A20 Row: G Column: 11  
 Seq primer: AGCGATACAAATTCACACAGA  
 High quality sequence stop: 534.  
 Location/Qualifiers

## FEATURES

Source

1. 534  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="BP230015A20G11"  
 /sex="female"  
 /lab\_host="DH10B"  
 /note="Organ: Placenta; Vector: pT73Pac; Site:1: EcorI;  
 Site:2: NotI; The cDNA library was contributed by the  
 Soares laboratory and it was constructed and normalized  
 as described by Bonaldo, M.F., Lennon, G. and Soares,  
 M.B. (1996), Genome Research 6(9): 791-806."  
 BASE COUNT 76 a 213 c 184 g 81 t  
 ORIGIN

## alignment\_scores:

Quality: 874.50 Length: 179  
 Ratio: 5.332 Gaps: 1  
 Percent Similarity: 91.620 Percent Identity: 85.475

## alignment\_block:

US-09-006-352-2 x AM464298 ..

Align seg 1/1 to: AM464298 from: 1 to: 554

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20 AAlaLeuProValProAlaValArgly...ValAlaGluThrProth 35
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
16 GCGTGGCTGCTGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCAT 65
35 rTyrrProTrpArgAspAlaGluThrGlyGlyAlaGlyValAlaGlnC 52
66 CTAACCGGTGAGGAGGACGAGAGCGGGGAGTGGCTGGTGGAGCAAGT 115
52 ysrProProGlyThrPheValAlaGlnArgProCysArgAspSerProThr 68
116 GCGCTCCGGGCGACCTTGTGCGAGCGCGCTTGGCGCGGAACGCCCAAG 165
69 ThrcysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrle 85
166 ACCTGGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 215
85 ugiuArgCysArgTyrCysAsnValLeuGlyGlyAlaGluThrGlnGlu 102
216 GAGGCGCTGCGCGCTGCTGCAACGTCATCTGCGGGAGCGCGAGGAGAG 265
102 laArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrly 118
266 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 315
113 PhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysProProG1 135
316 TTCTTGAGACAGCGCGCGCTGCTGAGACAGCGCTGCTGCGCGCGCG 365
135 yAlaGlyValAlaLeuProGlyThrProSerGlnAsnThrGlnCysGlnP 152
366 CCGCGCGCGGTGCTGCTCCGCGCGCGCGCGCGCGCGCGCGCGCG 415
152 rOCysProProGlyThrPheSerAlaSerSerSerSerSerGlnGlnCys 168
416 CCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 465
169 GlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProG1 185
466 CAGCCCGACCGCACTGCACAGCGCTGGCGCTGGCGCTGCATATGTGCTGG 515

```

185 ysrSerSerHisAspThrLeuGlyThrSerCysThr 197  
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 516 CTCCCGCTACAGCAGCGCGCTGTGACCACTGCAGC 552

seq\_name: gb\_est80:BE873766

seq\_documentation\_block:

LOCUS BE873766 697 bp mRNA 20-OCT-2000  
 DEFINITION 60148315F1 NIH\_MGC\_69 Homo sapiens cDNA clone IMAGE:3886635 5',  
 mRNA sequence.  
 ACCESSION BE873766  
 VERSION BE873766.1 GI:10322542  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE NIH-MGC <http://mgi.ncl.nih.gov/>  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)  
 Tissue Procurement: DCD/DIT/Gazdar  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LAM9663 Row: m Column: 04  
 High quality sequence stop: 675.  
 Location/Qualifiers

## FEATURES

Source

1. 697  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3886635"  
 /clone\_lib="NIH\_MGC\_69"  
 /issue\_type="large cell carcinoma, undifferentiated"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: Lung; Vector: pCMV-SPORT6; Site:1: NotI;  
 Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.1 kb. Library constructed by Life  
 Technologies."  
 BASE COUNT 112 a 245 c 224 g 115 t 1 others  
 ORIGIN

## alignment\_scores:

Quality: 868.00 Length: 186  
 Ratio: 5.017 Gaps: 3  
 Percent Similarity: 93.011 Percent Identity: 90.323

## alignment\_block:

US-09-006-352-2 x BE873766 ..

Align seg 1/1 to: BE873766 from: 1 to: 697

```

1 MetArgAlaLeuGluGlyProGlyLeuSerLeuGlyValAlaGluThrP 17
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
79 ATGAGGGCGCTGAGGAGGCGCGCTGCTGCTGCTGCTGCTGCTGGC 128
17 aLeuProAlaLeuLeuProValProAlaValArgGlyValAlaGluThrP 34
129 GCTGCTGCGCTGCTGCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCG 178
34 rOrhTyrrProTrpArgAspAlaGluThrGlyGlyAlaGlyValAlaGln 50
179 CCACCTACCGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 228
51 GlnCysProProGlyThrPheValAlaGlnArgProCysArgAspSerP 67
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

```
229 CAGTGGCCCCAGGACCTTTGTGACGGCG.TGCCGCCAGACAGCCC 277
67 oThrThcCysGlyProCysProPArgHisTyrThcInPheTrpAsnT 84
|||||
278 CAGACGCGTGGCCGTGTCCAGCGGCACCTACACGAGCTTGGAACT 327
84 yTLeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGlu 100
|||||
328 ACCTGGAGCGCTGCTACTGCAACGCTCTCGGGAGCGTAGAGAG 377
101 GluAlaArgAlaCysHisAlaThcHisAsnArgAlaCys...ArgCysAr 116
|||||
378 GAGGACAGCGGCTGCCAGCCACC.....AAACCGTCCGTCGCCGTGCG 421
116 gThcGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysP 133
|||||
422 CACGCGCTTCTTCGCGCAGCGTGTCTGCTTGGAGCAGCATCTGTC 471
133 rOPrOGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThcGln 149
|||||
472 CACCTGGTGGCGCGTATTGCCCCGGGACCCCGACGACAGACAGCAG 521
150 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerG 166
|||||
522 TGCCAGCGCGTCCCCCAGGACCTTCTCAGCAGCAGCAGCTCCTCAA 571
166 uGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsn 183
|||||
572 GCACTGGCAGNCC.CACCGAATGCACGGCCT...GGGCTTGCCCTCATG 617
183 aLProGly 185
|||||
618 TGCCAGGT 625
```

seq\_name: gb\_est42:AW083241

seq\_documentation\_block:

LOCUS AW083241 692 bp mRNA EST 14-OCT-1999  
DEFINITION xc07a04.x1 NCI-CGAP Co21 Homo sapiens cDNA clone IMAGE:2583534 3',  
similar to TR:095407 095407 DECOY RECEPTOR 3.; contains 1L.b1 MER22  
repetitive element.; mRNA sequence.

ACCESSION AW083241 GI:6038393

VERSION AW083241.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 692)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index

COMMENT Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cgaps-remail.nih.gov

TISSUE Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/BLN at:

www.bio.lnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 414.

Location/Qualifiers

1. 692

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2583534"

/clone\_lib="NCI-CGAP-Co21"

/tissue\_type="moderately differentiated adenocarcinoma"

/lab\_host="DH10B"

/note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Normalized to cot >500. Average insert size 1.04kb.  
by Life Technologies."

BASE COUNT 136 a 205 c 235 g 115 t 1 others

alignment\_scores:

Quality: 865.50 Length: 199  
Ratio: 4.678 Gaps: 2  
Percent Similarity: 92.965 Percent Identity: 88.945

alignment\_block:

us-09-006-352-2 x AW083241/rev ..

Align seg 1/1 to reverse of: AW083241 from: 1 to: 692

```
103 ArgAlaCysHisAlaThcHisAsnArgAlaCysArgCysArgThcGlyPh 119
|||||
689 CGGTCCGACGCGCTTCCAGCAGCAGCAGCAGCTGCTCCATCCGCGCAGGTT 640
119 ePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysProProGlyA 136
|||||
639 TTTTGGCAGCGCTG...TTTCTGCTGAGCAGCAGCATCTGCTCACCTGT 594
136 IaGlyValIleAlaProGlyThrProSerGlnAsnThcGlnGlyAsnPro 152
|||||
593 CGGCGTGATTTGCCCCGGGACCCAGTCCAGAACACCCAGTGGCCAGCG 544
153 CysProProGlyThrPheSerAlaSerSerSerSerSerGlnGlyCysG 169
|||||
543 TGCCCCCAGGACCTTCTCAGCAGCAGCAGCTCAGCTAGAGCACTGCCA 494
169 nProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGly 186
|||||
493 GCCCAGCAGCAACTGCACAGCGCCCTGGCCCTCAATGTGCAGAGCT 444
186 eRserSerHisAspThcLeuCysThrSerCysThcGlyPheProLeuSer 202
|||||
443 CTCTCTCCATGACACCTGTGCACAGCAGCTGCTGCTGCTGCTGCTGAGC 394
203 ThrArgValProGlyAlaGluGluCysGluArgAlaValIleAspPheVa 219
|||||
393 ACCAGGATCCAGGACGCTGAGAGAGTGTAGCGCTGCCGATCAGACTTTGT 344
219 AlaPheGlnAspIleSerIleLysArgLeuGlnArgLeuGlnAlaL 236
|||||
343 GCGTTTCCAGGACATCTCCATCAGAGAGCTGACGCGCTGCTGCAGAGGCC 294
236 eUGluAlaProGlyGlyTrpGlyProThrProArgAlaGlyArgAlaLa 252
|||||
293 TCGAGGCCCCCGAGGCGTGGGCTCCGACACAGGCGCGCGCGGCC 244
253 LeuGlnLeuLysLeuArgArgArgLeuThcGluLeuLeuGlyAlaGlnA 269
|||||
243 TTGCAAGCTGAAACTTGGCTCGCGGCTTACGAGAGCTCTGGGGGCGCAGG 194
269 sPGlyAlaLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMet 285
|||||
193 ACGGGGCGCTCTGTGGCGCTGCTGCAGGCGCTGCGCGCGCGCCAGGATG 144
286 ProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 300
|||||
143 CCGCGGCTGAGAGCGAGCGTCCGTGAGCGCTTCTGCTGTCAC 99
```

seq\_name: gb\_est44:AW262121

seq\_documentation\_block:

LOCUS AW262121 600 bp mRNA EST 28-DEC-1999  
DEFINITION xq31d04.x1 NCI-CGAP Lu28 Homo sapiens cDNA clone IMAGE:2752231 3',  
similar to TR:095407 095407 DECOY RECEPTOR 3.; contains TPRI.b1





Mon Nov 5 08:22:44 2001

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Page 8

```

VERSION      AM662363.1  GI:7454901
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 514)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished (1997)
JOURNAL      Contact: Robert Strausberg, Ph.D.
              Email: rgs@ebi.ac.uk
COMMENT      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
              Emmert-Buck, M.D., Ph.D.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: Greg Lennon, Ph.D.
              Clone distribution: NCI-CGAP clone distribution Information can be
              found through the I.M.A.G.E. Consortium/ILNt at:
              image.llnl.gov/image/html/resources.shtml
              Seq. primer: -400P from glibco
              High quality sequence stop: 368.
FEATURES
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        1..514
            location/Qualifiers
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone IMAGE:2973337
                /clone_id="NCI_CGAP_Co14"
                /tissue_type="moderately-differentiated adenocarcinoma"
                /lab_host="DH10B"
                /note="Organ: colon; Vector: PCMW-SPORT6; Site_1: Salt;
                Site_2: NCI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 1.7 kb. Life Technologies catalog #:
                11531-019"
BASE COUNT    113 a      156 c      159 g      85 t      1 others
ORIGIN
Alignment_scores:
    Quality: 653.00      Length: 131
    Ratio: 5.102        Gaps: 0
    Percent Similarity: 97.710      Percent Identity: 97.710
Alignment block:
    US-09-006-352-2 x AM662363/rev ..
Align seg 1/1 to reverse of: AM662363 from: 1 to: 514
170 ProHtsArgAsnCyThrAlaLeuGlyLeuAlaLeuAsnValProGlyse 186
|||||
514 CCCCACAGCAACTGACAGGGCTGGGGCTGGCCCTCAATATGGCCAGGCTC 465
186 rSetSerHisAspThrLeucysThrsertCysThriglypHeProLeuSert 203
464 TTCTCTCCATGACACCCNTGTGCACCAAGCTGACACTGGCTTCCCTCCAGCA 415
203 hraTValProGlyAlaGluLucySGuAuaTAlaValIleaspPheVal 219
414 CCAGGAGTACAGAGAGCTGAGAGATGTGACCGCTCATGACACTTGTG 365
220 AlaPheGlnAspIleSerIleLysArgLeuGlnAArgLeuGlnAlaLe 236
364 GCTTTCACAGGACATCTCCATCAAGAGGCTGCGCGGCTGCGAGGCGCT 315
236 uGluAlaProGluGlyTTrpGlyProThrProArgAlaGlyTArgAlaL 253
314 CGAGCGCCCGCAGGCGCTGGGGTCCGACACCAAGGCGCGGCGCGCGCT 265
253 eugInLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnASP 269
|||||
264 TCGAGCTGAAGCTGCTCGCGCGCTCAGGAGCACTCTCTGGGGCGCCAGGAC 215

```

```

seq_name: gb-est24:AT18743
seq_documentation_block: 475 bp mRNA EST 10-JUN-1999
LOCUS AT18743
DEFINITION aassn04.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE: J2353399 3', mRNA sequence.
ACCESSION AT18743
VERSION AT18743.1 GI:5035999
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 475)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Gelsel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Martin,J.,
Moore,B., Schellenberg,K., Stepien,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
Washington University NCI Human EST Project
Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box B501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNCr; contact the
IMGE Consortium (info@imge.llnl.gov) for further information.
Seq primer: -40UP from Glbpco
High quality sequence stop: 467.
Location/Qualifiers
1 475
FEATURES
source /organism="Homo sapiens"
/db_xref="taxon:9606"
/cclone_image=J2353399"
/cclone_lib=Barstead aorta HPLRB6"
/sex="male"
/dev_stage="adult, age 64"
/lab_host="DH10B (phage resistant)"
/note="Organ: aorta; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTGAGCATCTGTGAAGTCGAGCGGGCCGCCCTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[5' AATTGCATCGAAC 3' and 5' GTTGGATCGG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library constructed by Bob
Barstead."
BASE COUNT 98 a 153 c 151 g 73 t
ORIGIN
Alignment_scores:
Quality: 644.00 Length: 127
Ratio: 5.071 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-006-352-2 x AT18743/rev ...
Align seg 1/1 to reverse of: AT18743 from: 1 to: 475
174 CysThAlaLeuGlYleuAlaIalaAsnValProGlySerSerHis 190
|||||
473 TGcAcGccCtTGgcCtGgCcCtCAAtGcTgcCAGgcCtTtCtCCcAATA 424

```

190 pphrleucythrsercysrthglypheproleuserthrargvalpro 207  
|||||  
423 CAGCGCTGCACGAGCTGCACGCTCTCCCTCCACACAGGCTACGAC 374  
207 1yalaaglucysgluargalavalileasphevalialaphegnasp 223  
|||||  
373 GAGCTGAGGAGTGTAGCTGCTGCTATCATGACTTGTGCTTCCAGGAC 324  
224 1leaserileysargleuaglnargleuaglnalaleuaglialaprosl 240  
|||||  
323 ATCTCATCAAGAGGCTGCAGCGCTGCTGCAAGGCCCTGAGAGCCCGCA 274  
240 ugltyrpeglyprothrproargalaglyargalalaleuaglnleuyls 257  
|||||  
273 GGGCTGGGGTCCGACACCAAGGCGGCCCGCGCTTGACAGCTGAAGC 224  
257 euargargleuthrgleuaglnleuaglyalaglnaspglyalaleu 273  
|||||  
223 TCGCTGGGCGCTCACGAGCTCTGGGGGCGAGAGCGGCGCTGCTG 174  
274 valargleuaglnalaleuargvalalargmetproglyleuagluar 290  
|||||  
173 GGGCGCTGCTGCAGGCGCTGGCGGCGCAGATGCCGGCTGAGCG 124  
290 gservalarggluarphleuprovalhis 300  
|||||  
123 GAGGCTCCGTGAGCGCTTCTCCCTGTCAC 93  
seq\_name: gb\_est82:BF001490

seq\_documentation\_block: 478 bp mRNA EST 06-OCT-2000  
LOCUS BF001490 798810.x1 NCI\_CGAP\_Col6 Homo sapiens cDNA clone IMAGE:3313603 3'  
DEFINITION similar to contains PFR5, b1 TAR1 repetitive element ;, mRNA  
sequence.  
ACCESSION BF001490  
VERSION BF001490.1 GI:10701765  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 478)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapds-remail.nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,  
Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL, send email to:  
info@image.lnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 419.  
Location/Qualifiers

FEATURES  
source  
1..478  
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/db\_xref="taxon:9606"  
/clone="IMAGE:3313603"  
/clone\_lib="NCI\_CGAP\_Col6"  
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/lab\_host="DH10B"  
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Plasmid DNA from the normalized library NCI\_CGAP\_Col6 was  
prepared, and as circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(cloneids 1057416-1061255, and 114584-114531).  
Subtraction by Bento Soares and M. Fatima Bonaldo. "

alignment\_scores:  
Quality: 604.00 Length: 119  
Ratio: 5.076 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-006-352-2 x BF001490/rev ..

Align seg 1/1 to reverse of: BF001490 from: 1 to: 478

182 Asnvalproglyseraserhisasprhrleucythrsercysrthrgl 198  
|||||  
476 AATGTGCCAGGCTTCCCTCCATGACACCTGTCAGCAGCTGCACTGG 427  
198 ypheproleuserthrargvalproglyalaglucysgluargalav 215  
|||||  
426 CTTCCCTCCACACAGGAGGTACAGAGCTGAGAGTGTAGAGCTGCCG 377  
215 alileasphvealialaphegnaspilaserileysargleuaglnar 231  
|||||  
376 TCATCGACTTGTGTGCTTCCAGAGCATCTCATCAAGAGGTGACGCG 327  
232 leuaglnalaleuaglnalaprogluyltrpglyprothrproargal 248  
|||||  
326 CTGCTGCAGGCGCTCGAGGCCCGAGAGGTGGGTCCGACACCAAGGCG 277  
248 aglyargalalaleuaglnleuylsleuargargleuthrgleuul 265  
|||||  
276 GGGCGCGCGGCGCTTGCAGCTGACCTGTGGGCGCTGACAGAGCTCC 227  
265 euaglialaglnaspglyalaleuvalargleuaglnalaleuarg 281  
|||||  
226 TGGGCGCGCAGCAGCGGCGCTGCTGTGGCTCTGCTGAGCGCTGCGC 177  
282 valalargmetproglyleuaglnarservalarggluarphleupr 298  
|||||  
176 GGGCGCAGAGATGCCGGGCTGAGCGAGCGTCCGTGACCTTCTCC 127  
298 ovalhis 300  
|||||  
126 TGTGCAC 120  
seq\_name: gb\_est42:AM083914

seq\_documentation\_block: 515 bp mRNA EST 14-OCT-1999  
LOCUS AM083914 xc25502.x1 NCI\_CGAP\_Col9 Homo sapiens cDNA clone IMAGE:2585330 3'  
DEFINITION similar to TR:095407 095407 DEOY RECEPTOR 3.;, mRNA sequence.  
ACCESSION AM083914  
VERSION AM083914.1 GI:6039066  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 515)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapds-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life  
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)  
Seq primer: -400p from Gibco  
High quality sequence stop: 355.

## FEATURES

Source  
Location/Qualifiers  
1..515  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NCI-CGAP\_Col9"  
/tissue\_type="moderately differentiated adenocarcinoma"  
/lab\_host="DH10B"  
/note="Organ: Colon; Vector: pCMV-Sport6; Site\_1: Salt;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Normalized to Cot 50. Average insert size 1.32kb.  
Normalized version of NCI-CGAP\_Col8. Library constructed  
by Life Technologies."  
BASE COUNT 102 a 160 c 158 g 94 t 1 others  
ORIGIN

alignment\_scores:  
Quality: 584.00 Length: 137  
Ratio: 4.598 Gaps: 0  
Percent Similarity: 92.701 Percent Identity: 92.701

## alignment\_block:

US-09-006-352-2 x AM083914/rev

Align seg 1/1 to reverse of: AM083914 from: 1 to: 515

```
164 SerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGluLeuAla 180
|||||
515 AGCTCAGAGCAGTCAGCCCGCCGCAAMTGCAGCCCTGTGGCTGGCGC 466
180 AlaAsnValProGlySerSerHisAspThrLeuGlySerCysT 197
|||||
465 CCTCATGTGCGCAGGCTCTTCTCCCAATGACACCTGTGACACCTTCCA 416
197 htcGlyPheProLeuSerThrArgValProGlyAlaGluGluGlyGlu 213
|||||
415 CTGGCTTCCCTCAGCAGCAGGGTACAGAGCTGAGAGGTGAGCGCT 366
213 AlaValIleAspPheValAlaPheGlnAspIleSerIleValArgLeuG 230
|||||
230 nargLeuLeuGlnAlaLeuGlnAlaProGluGlyTyrProGlyProPro 247
|||||
316 GCGCGTGTGCGAGCCCTCGAGGCCCGGAGGGCTGGGGTCCGACACA 268
247 rgaIaGlyArgAlaAlaLeuGlnLeuGlnArgArgArgLeuGlnGlu 263
|||||
267 GGGCGGGGCGCGGCGCTTGCAGCTGAGCTGCGCGCGCTCACGAG 218
264 LeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuGlnAla 280
|||||
217 CTCTCGGGGGCGCAGCAGCGGCGCTGCTGGCGCTGTGAGGCGCT 168
280 uatGValAlaArgMetProGlyLeuGluArgSerValArgGluArgPhe 297
|||||
167 GCGCGTGGCGCAGATGCCGGGCTGGAGCGAGAGTCCGTGAGACGCTTC 118
297 eupProValHis 300
|||||
117 TCCCTGTGCAC 107
```

seq\_name: gb\_est41:AM014771

seq\_documentation\_block:

LOCUS AM014771 459 bp mRNA EST 10-SEP-1999  
DEFINITION UI-H-BIO-aag-g-04-0-01.s1 NCI-CGAP-Sub1 Homo sapiens cDNA clone  
IMAGE:2709294 3', mRNA sequence.

ACCESSION AM014771  
VERSION AM014771.1 GI:5863528

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
1 (bases 1 to 459)  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

TITLE Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Email: Robert Strausberg, Ph.D.  
Contact: cgaps@mail.nih.gov  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)  
Seq primer: M13 Forward  
POLY-A=yes.

FEATURES  
Source  
Location/Qualifiers  
1..459  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/clone\_lib="NCI-CGAP-Sub1"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT730-pac (Pharmacia) with a modified  
polylinker. Site\_1: Not I; Site\_2: Eco RI; The  
NCI-CGAP-Sub1 library is a subtracted library derived from  
BI. BI constitutes a mixture of 21 normalized or  
subtracted NCI-CGAP libraries: NCI-CGAP\_Col4  
NCI-CGAP\_P122, NCI-CGAP\_P128, NCI-CGAP\_Col10, NCI-CGAP\_Col16  
NCI-CGAP\_P125, NCI-CGAP\_P182, NCI-CGAP\_P183,  
NCI-CGAP\_Kid5, NCI-CGAP\_Kid12, NCI-CGAP\_Kid3,  
NCI-CGAP\_Kid11, NCI-CGAP\_LyM2, NCI-CGAP\_B12, NCI-CGAP\_Col8,  
NCI-CGAP\_Col1, NCI-CGAP\_L612, NCI-CGAP\_B123, NCI-CGAP\_Lu5  
, NCI-CGAP\_Lu24, NCI-CGAP\_Lu19, NCI-CGAP\_G64, NCI-CGAP\_G66  
, NCI-CGAP\_B125. These 21 libraries were pooled and a  
single-stranded DNA preparation of the resulting mixture  
was used as a tracer in a subtractive hybridization with a  
driver whose composition is detailed below: NCI-CGAP\_Kid3  
pool 1 L1AM 3334-3337, 3682-3683, 3798-3803 (IMAGE  
Cloneids 1322376-1323911, 1456008-1456775, 1500552-1502855  
) NCI-CGAP\_Kid5 pool 1 L1AM 3338-3342, 3722-3725,  
3776-3778 (IMAGE Cloneids 1333912-1325831,  
1471368-1472903, 1492104-1493255) NCI-CGAP\_Lu5 pool 1 L1AM  
3575-3582, 3851-3854 (IMAGE Cloneids 141920-1417991,  
1520904-1522439) NCI-CGAP\_G64 pool 1 L1AM 3164-3167,  
3716-3720, 3733-3735 (IMAGE Cloneids 1257096-1258631,  
1460064-1470983, 1475592-1476743) NCI-CGAP\_P122 pool 1  
L1AM 2457-2459, 2758-2759, 3062-3068 (IMAGE Cloneids  
985608-986759, 1101197-1101959, 1217928-1220615)  
NCI-CGAP\_Col10 pool 1 L1AM 2644-2653, 2871-2872 (IMAGE  
Cloneids 1057416-1061255, 1144584-1145351) The resulting  
subtracted library contained 530,000 recombinants.  
Lennon & Soares (1996): Normalization and subtraction:  
Two Approaches To Facilitate Gene Discovery. Genome  
Research 6, 791-806.  
TAG\_L1B=NCI-CGAP\_Col4  
TAG\_TISSUE=colon  
TAG\_SEQ=CTTGC"

BASE COUNT 93 a 143 c 136 g 87 t

ORIGIN

alignment\_scores:



Quality: 580.00 Length: 116  
Ratio: 5.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 98.276

## alignment\_block:

US-09-006-352-2 x AW014771/rev ..

Align seg 1/1 to reverse of: AW014771 from: 1 to: 459

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185 GlySerSerHisAspThrLeuCysThrSerCysThrGlyPheProLe 201
|||||
457 GGCTTCCTCCATGACACCCCTGTCACACGACGACTGGCTTCCCTC 408
201 uSerThrArgValProGluAlaGluCysGluArgAlaValIleasp 218
|||||
407 CAGCACCGAGGTACAGAGAGCTGAGAGTGTGACCTCATGAGACT 358
218 heValAlaPheGlnAspIleSerIleLysArgLeuGlnArgLeuGln 234
|||||
357 TTGTGGCTTCCAGGACATCTCCATCAAGAGCTGACGCGGTTCTGCGAG 308
235 AlaLeuGlnAlaProGluGlyTrpGlyProThrProArgAlaGlyArgAl 251
|||||
307 GCCCTTCAGAGCGCCGAGAGGCTGGGGTCCGACACCAAGGCGGCGCGC 258
251 aAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaG 268
|||||
257 GGCTTCAGCTGAAGCTGCGTCCGCGGCTCAGAGAGCTCTGGGGGCGC 208
268 InaAspGlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArg 284
|||||
207 AGGAGGCGGCGCTCTGTCGCGCTGTCGAGGCGCTGCGGTCGCCAGG 158
285 MetProGlyLeuGlnArgSerValArgGluArgPheLeuProValHis 300
|||||
157 ATGCCCGGCGCTGAGCGAGCGCTCCGTGAGCGCTTCTCTCTGTGCAC 110
```

seq\_name: gb\_est25:AI857725

## seq\_documentation\_block:

LOCUS AI857725 445 bp mRNA EST 07-MAR-2000  
DEFINITION w121a08.x1 NCI\_CGAP\_Ut1 Homo sapiens CDNA clone IMAGE:2425526 3',  
mRNA sequence.  
ACCESSION AI857725  
VERSION AI857725.1 GI:5511330  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.

## JOURNAL

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
Insert Length: 1138 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence size: 418.

## FEATURES

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1. .445  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2425526"

/clone\_lib="NCI\_CGAP\_Ut1"  
/tissue\_type="well-differentiated endometrial  
adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Life Technologies catalog #:  
11538-014"

BASE COUNT 100 a 140 c 130 g 75 t  
ORIGIN

## alignment\_scores:

Quality: 546.00 Length: 108  
Ratio: 5.056 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-006-352-2 x AI857725/rev ..

Align seg 1/1 to reverse of: AI857725 from: 1 to: 445

```
193 CysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaG 209
|||||
445 TGACACCACTGCACCTGCTCCCTCCAGACACGACGTAACAGAGGCTGA 396
209 uGluCysGluArgAlaValIleaspPheValAlaPheGlnAspIleSer 226
|||||
395 GGAGGTGAGCGTGGCTCATCGACTTGTGTGCTTCCAGGACATCTCCA 346
226 IeLysArgLeuGlnArgLeuLeuGlnAlaLeuGlnAlaProGluGlyTrp 242
|||||
345 TCAGAGAGCTGACAGGCGCTGCTGACAGGCTCGAGGCGCCGAGAGGCTGG 296
243 GlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysArgArg 259
|||||
295 GGTCCGACACCAAGGCGGCGCGCGCTTGCAGCTGAAGCTGCGTCG 246
259 ArgLeuThrGlnLeuLeuGlnAlaGlnAspGlyAlaLeuLeuValArgL 276
|||||
245 GCGGCTCAGGAGGCTCCTGGGGGCGCAGAGCGGCGCTGCTGTGCGCGC 196
276 euleuGlnAlaLeuArgValAlaArgMetProGlyLeuGluArgSerVal 292
|||||
195 TGCTGCAAGCGCTGCGCGTGGCCAGAGATGCCCGGCGTGGAGCGAGCGTC 146
293 ArgGluArgPheLeuProValHis 300
|||||
145 CGTGAAGCGCTTCTCTCCCTGTGCAC 122
```

Mon Nov 5 08:22:44 2001

us-09-006-352-2.rst

Page 12

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2001, 12:32:46 ; Search time 19.91 Seconds  
(without alignments)  
913.470 Million cell updates/sec

Title: US-09-006-352-2  
Perfect score: 1634  
Sequence: 1 MRALEGPGLSLCLVLALPA.....RVARMPGLERSVREPLFVH 300

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues  
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_0601:\*

- 1: /SIDSL/gcgdata/geneseq/geneseqp/AA1980.DAT:\*
- 2: /SIDSL/gcgdata/geneseq/geneseqp/AA1981.DAT:\*
- 3: /SIDSL/gcgdata/geneseq/geneseqp/AA1982.DAT:\*
- 4: /SIDSL/gcgdata/geneseq/geneseqp/AA1983.DAT:\*
- 5: /SIDSL/gcgdata/geneseq/geneseqp/AA1984.DAT:\*
- 6: /SIDSL/gcgdata/geneseq/geneseqp/AA1985.DAT:\*
- 7: /SIDSL/gcgdata/geneseq/geneseqp/AA1986.DAT:\*
- 8: /SIDSL/gcgdata/geneseq/geneseqp/AA1987.DAT:\*
- 9: /SIDSL/gcgdata/geneseq/geneseqp/AA1988.DAT:\*
- 10: /SIDSL/gcgdata/geneseq/geneseqp/AA1989.DAT:\*
- 11: /SIDSL/gcgdata/geneseq/geneseqp/AA1990.DAT:\*
- 12: /SIDSL/gcgdata/geneseq/geneseqp/AA1991.DAT:\*
- 13: /SIDSL/gcgdata/geneseq/geneseqp/AA1992.DAT:\*
- 14: /SIDSL/gcgdata/geneseq/geneseqp/AA1993.DAT:\*
- 15: /SIDSL/gcgdata/geneseq/geneseqp/AA1994.DAT:\*
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- 21: /SIDSL/gcgdata/geneseq/geneseqp/AA2000.DAT:\*
- 22: /SIDSL/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1634	100.0	300	19	AAW66102
2	1634	100.0	300	19	AAW63622
3	1634	100.0	300	20	AAI03099
4	1634	100.0	300	20	AAI42182
5	1634	100.0	300	20	AAI17479
6	1634	100.0	300	20	AAV06817
7	1634	100.0	300	20	AAW97749
8	1634	100.0	300	20	AAW95082
9	1634	100.0	300	21	AAI19335
10	1634	100.0	300	21	AAI28559
11	1634	100.0	300	21	AAI24057

12	1634	100.0	300	21	AAI33416	Human PRO212 prote
13	1634	100.0	300	21	AAI30621	Human Fas ligand 1
14	1634	100.0	300	21	AAI97246	M68 TNF receptor 1
15	1634	100.0	300	21	AAI90357	Human tumour necro
16	1634	100.0	300	21	AAI24395	Human PRO212 prote
17	1634	100.0	300	21	AAI96596	Human FLINT. Homo
18	1634	100.0	300	22	AAI74466	Human FLINT native
19	1634	100.0	300	22	AAI71754	Human NTR3. Homo
20	1634	100.0	300	22	AAI48161	Human PRO212 poly
21	1634	100.0	300	22	AAI50903	Human PRO212 prote
22	1620	99.1	300	21	AAI77458	Human TNF receptor
23	1619	99.1	300	21	AAI19710	Human FAS ligand 1
24	1619	99.1	300	21	AAI96597	Human FLINT. Homo
25	1610	98.5	302	20	AAI42183	Human FLINT #2 pro
26	1509	92.4	300	21	AAI803623	Human Fas ligand 1
27	1502	91.9	300	21	AAI803622	Monkey Fas ligand
28	1502	91.2	300	21	AAI803624	Human Fas ligand 1
29	1491	91.2	271	20	AAI42184	Human mFLINT #1 pr
30	1491	91.2	271	21	AAI19334	A mature human Fas
31	1491	91.2	271	21	AAI19705	Human FAS ligand 1
32	1491	91.2	271	21	AAI97247	M68 TNF receptor r
33	1491	91.2	271	21	AAI96598	Human mature FLINT
34	1491	91.2	271	22	AAI74465	Human FLINT mature
35	1487	91.0	271	21	AAI19709	Protease-resistant
36	1487	91.0	271	22	AAI74467	Human FLINT mature
37	1485	90.9	271	21	AAI96599	Human mature FLINT
38	1481	90.6	271	21	AAI19708	Protease-resistant
39	1475	90.3	271	21	AAI19706	Protease-resistant
40	1467	89.8	271	21	AAI19707	Human mFLINT #2 pr
41	1467	89.8	273	20	AAI42185	Human tumour nec
42	1362	82.0	245	20	AAI28449	A human soluble TNF
43	1177	72.0	211	21	AAI28560	Human soluble TNF
44	1153	70.6	215	20	AAI93585	Human hAP6 protei
45	841	51.5	153	20	AAI22222	Human TNFR superfa

#### ALIGNMENTS

RESULT 1

AAW66102 standard; Protein; 300 AA.

AC AAW66102;

XX

DT 03-DEC-1998 (first entry)

XX

DE Amino acid sequence of tumour necrosis related receptor (TR4).

XX

KW Human; tumour necrosis related receptor; TR4; agonist; antagonist;

KW Inhibition; chronic; acute; inflammation; arthritis; septicemia;

KW autoimmune disease; transplant rejection; stroke; cancer;

KW Alzheimer's disease.

XX

OS Homo sapiens.

OS

XX

PN EP861850-A1.

PD 02-SEP-1998.

XX

PE 20-JAN-1998; 98EP-0300382.

XX

PR 04-FEB-1997; 97US-0794796.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Emery J, Tan KB, Truneh A, Young PR;

XX

DR WPL: 1998-508248/44.

XX

DR N-PSDB; AAV07654.

XX

PT New DNA encoding tumour necrosis related receptor - used to treat

PT and prevent e.g. inflammation, arthritis, septicemia, autoimmune

PT diseases, transplant rejection, infection, stroke, ischemia, ARDS,  
PT restenosis, AIDS, bone disorders and cancer  
XX  
XX Claim 1; Fig 1; 21pp; English.  
XX  
CC This is the amino acid sequence of the human tumour necrosis related  
CC receptor (TR4) used in the method of the invention. The TR4 protein  
CC or its agonist can be used to treat a subject in need of enhanced  
CC TR4 polypeptide activity. The antagonist is used to inhibit TR4  
CC polypeptide activity. The active agents can be used for the  
CC treatment and prevention of diseases such as chronic and acute  
CC inflammation, arthritis, septicemia, autoimmune diseases, transplant  
CC rejection, stroke, cancer, Alzheimer's disease.  
XX  
SQ Sequence 300 AA:  
  
Query Match 100.0%; Score 1634; DB 19; Length 300;  
Best Local Similarity 100.0%; Pred. No. 5.8e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRALGPGLSLCLVLAIPALPVPVAVGAEPTYPWMDAETGERLYCAACPPGTAYOR 60  
DB 1 mralepgslslclvialpalpvpavryvaeetpymrdaetgerlycagcpptgtvqr 60  
QY 61 PCRDSPTTCGPPRRHYTOFWNYLERCRYCNVLCGEREEARACHATHNRACRRTGFF 120  
DB 61 pcrdspttcgpprrhytqfwylercrycnvlgereearachathnrcrctgff 120  
  
QY 121 AAAGCLEHASCPPGAGVIAGTPSONTOCOPCPPTGFSASSSSSEOCQPHRNCTALGLA 180  
DB 121 ahagiclehaescppgagviagtpsqntqcpqppgtfsassssseqqphrntaigla 180  
QY 181 LNVPGSSSHDPLTCTGTFPLSTRVPGAECCEERAVIDFAFODISIKRLOALBAPE 240  
DB 181 lnvpgssshdltctscgtfplstrvgaecceeravidfaafdisikrlqllqaleape 240  
QY 241 GWCPTPRAGRALQKLRRLRTELIGAOGALLVRLQLARVARNPGERSVRRFLPVH 300  
DB 241 gwcptpragralqklrrrtelllgagdgallvrlqlarvampgiersvrerflpvh 300  
  
RESULT 2  
AAW63622 standard; Protein; 300 AA.  
ID AAW63622  
XX  
AC AAW63622;  
XX  
DT 26-OCT-1998 (first entry)  
XX  
DE Human tumour necrosis factor receptor-6 alpha protein.  
XX  
XX Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;  
KW endothelial cells; keratinocytes; normal prostate; apoptosis;  
KW prostate tumour tissue.  
XX  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..30  
FT Protein 31..300  
FT /note="TNFR-6 alpha"  
FT Region 31..282  
FT /note="Soluble extracellular domain"  
XX  
PN W09830694-A2.  
XX  
PD 16-JUL-1998.  
XX  
FE 13-JAN-1998; 98MO-US00153.  
XX  
PR 14-JAN-1997; 97US-0035496.  
XX

PA (HUMA-) HUMAN GENOME SCI INC.  
PI Ehnert R, Feng P, Gentz RL, Nt J, Ruben SM, Yu G;  
XX  
XX WPI: 1998-399142/34.  
DR N-PSDB; AAW39085.  
XX  
XX Human tumour necrosis factor receptors 6-alpha and 6-beta - used in  
PT the diagnosis of immune system-related disorder(s)  
XX  
XX Claim 20; Fig 1; 91pp; English.  
XX  
CC The present sequence represents the human tumour necrosis factor  
CC receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides  
CC for the TNFR-6 beta protein (AAW63623). TNFR-6 alpha and TNFR-6 beta  
CC are members of the tumour necrosis factor receptor (TNFR) family. TNFRs  
CC are expressed in endothelial cells, keratinocytes, normal prostate and  
CC prostate tumour tissue. For a number of disorders of these cells,  
CC particularly of the immune system, substantially altered (whether  
CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene  
CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta  
CC polypeptides, nucleic acids and antibodies are claimed to be useful in  
CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and  
CC also claimed to be useful for identifying ligands which may be useful  
CC in the treatment of apoptosis related disorders.  
XX  
SQ Sequence 300 AA:  
  
Query Match 100.0%; Score 1634; DB 19; Length 300;  
Best Local Similarity 100.0%; Pred. No. 5.8e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRALGPGLSLCLVLAIPALPVPVAVGAEPTYPWMDAETGERLYCAACPPGTAYOR 60  
DB 1 mralepgslslclvialpalpvpavryvaeetpymrdaetgerlycagcpptgtvqr 60  
QY 61 PCRDSPTTCGPPRRHYTOFWNYLERCRYCNVLCGEREEARACHATHNRACRRTGFF 120  
DB 61 pcrdspttcgpprrhytqfwylercrycnvlgereearachathnrcrctgff 120  
  
QY 121 AAAGCLEHASCPPGAGVIAGTPSONTOCOPCPPTGFSASSSSSEOCQPHRNCTALGLA 180  
DB 121 ahagiclehaescppgagviagtpsqntqcpqppgtfsassssseqqphrntaigla 180  
QY 181 LNVPGSSSHDPLTCTGTFPLSTRVPGAECCEERAVIDFAFODISIKRLOALBAPE 240  
DB 181 lnvpgssshdltctscgtfplstrvgaecceeravidfaafdisikrlqllqaleape 240  
QY 241 GWCPTPRAGRALQKLRRLRTELIGAOGALLVRLQLARVARNPGERSVRRFLPVH 300  
DB 241 gwcptpragralqklrrrtelllgagdgallvrlqlarvampgiersvrerflpvh 300  
  
RESULT 3  
AAV03099 standard; Protein; 300 AA.  
ID AAV03099  
XX  
AC AAV03099;  
XX  
DT 09-DEC-1999 (first entry)  
XX  
DE Human lung TNF-receptor protein.  
XX  
XX Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;  
KW detection; immunoassay; diagnosis; disease; immune system; tumour;  
KW osteogenic system; cardiovascular system; central nervous system; asthma;  
KW peripheral nervous system; transplant incompatibility; antitumor;  
KW rheumatoid arthritis; antiasthmatic; antiarthritic.  
XX  
XX Homo sapiens.  
OS  
XX

FH Key Location/Qualifiers  
 FT CDS 134..1036  
 FT /\*tag= a  
 FT /product= "TNF-receptor"  
 PN DE19809978-A1.  
 XX 16-SEP-1999.  
 PD 16-SEP-1999.  
 XX 09-MAR-1998; 98DE-1009978.  
 PF 09-MAR-1998; 98DE-1009978.  
 XX 09-MAR-1998; 98DE-1009978.  
 PA (BADI ) BASF AG.  
 PI Kroeger B;  
 XX WPI: 1999-519473/44.  
 DR N-PSDB; AA209998.  
 XX  
 PT New soluble member of tumor necrosis factor receptor family, useful for  
 PT identification specific modulators and for treating disease e.g. tumors  
 PT  
 PS Claim 1; Page 8-9; 10pp; German.  
 XX  
 XX This invention describes a novel tumour necrosis factor (TNF) receptor  
 CC (I) isolated from human lung tissue. (I) is used: (i) to raise specific  
 CC antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands  
 CC (A), potential therapeutic agents; and (iii) therapeutically (optionally  
 CC expressed from a gene therapy vector) in conditions associated with a  
 CC deficit of (I). Ab are used: (a) for qualitative or quantitative  
 CC detection of (I) in standard immunoassays (for diagnosis of disease, or  
 CC susceptibility, or for monitoring); and (b) as therapeutic inhibitors in  
 CC cases where (I) is overexpressed. Nucleic acid (II) that encodes (I) is  
 CC used: (A) for recombinant production of (I); (B) also its oligonucleotide  
 CC fragments, in standard hybridization and/or amplification assays; (C) as  
 CC source of antisense molecules or ribozymes; and (D) to produce transgenic  
 CC animals (for studying (patho)physiology of (I)). Diseases possibly  
 CC associated with under- or over-expression of (I) are those of the immune,  
 CC osteogenic, cardiovascular and central or peripheral nervous systems, the  
 CC tumors, transplant incompatibility, asthma and rheumatoid arthritis. The  
 CC products of the invention have antitumor, antiallergic and  
 CC antirheumatic activity. This sequence represents the TNF-receptor of the  
 CC invention.  
 CC  
 XX Sequence 300 AA:  
 SQ

Query Match 100.0%; Score 1634; DB 20; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 5,8e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALBPGSLICLVIALPALPVPVAVGVAEPTTPYPMRDATGERTIVCAQCPGGTFVQR 60  
 DB 1 mralepgslslclvialpallpvpavrgvaepttpyvmrdatgertivcagcpqpfivgr 60  
 QY 61 PCRBDSPTCGCPRRHYHGFWMYLERCRNVLCGEREEARACATNHRACRCRTGFF 120  
 DB 61 pcrtdspctcgprrhyhgfwmylecrncvlgereearacatnhracrcrtgff 120  
 QY 121 AHAGFCLIEHASCPPGAGVIAPGTSONTOCQPCPPTFSASSSSSSBOCQPHRMCTALGLA 180  
 DB 121 ahagfcliehascpvgagviapgtsonctqpcppptfssassssboqphrmctalgla 180  
 QY 181 LNVPGSSSHDFTCTSGTGPPLSTRVPGAECEERAVTDFVAFODISIKRLQRLQALPAPE 240  
 DB 181 lnvpgssshdftctsgtgpplstrvpgaeceeravidfvafigisikrlqllqaleape 240  
 QY 241 GAGPTPRAGRAALQLRLRLFTLLGADGALLVRLQALRVARMGLERSVERFLPVH 300  
 DB 241 gwpgtprragrraalqlrlrlftlllgadgallvrlqalrvarmglersverflpvh 300

RESULT 4  
 ID AA42182  
 XX AA42182 standard; Protein; 300 AA.  
 AC AA42182;

DE 17-DEC-1999 (first entry)  
 XX Human FLINT #1 protein sequence.  
 XX

KW Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;  
 KW apoptosis; inflammation; cancer; diabetes; acute liver failure;  
 KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;  
 KW reperfusion-associated injury; aplastic anaemia; differentiation;  
 KW growth; myelodysplastic syndrome; pancytopenic condition;  
 KW myocardial ischaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0950413-A2.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PF 30-MAR-1999; 99WO-US06797.  
 XX  
 PR 30-MAR-1998; 98US-0079856.  
 PR 20-MAY-1998; 98US-0086074.  
 PR 09-SEP-1998; 98US-0099643.  
 PR 17-DEC-1998; 98US-0112577.  
 PR 18-DEC-1998; 98US-0112703.  
 PR 18-DEC-1998; 98US-0112933.  
 PR 22-DEC-1998; 98US-0113407.  
 XX

PA (ELIL ) LILLY & CO ELI.

PI Bimol TF, Dou S, Glasbrook AL, Gould KE, Hale JE, Heuer JG;  
 PI Hul KY, Kharitonov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;  
 PI Song HY, Wang J, Wu X, Zuckerman SH;  
 XX  
 XX WPI: 1999-591319/50.  
 DR N-PSDB; AA25375.  
 XX

PT Use of mature FLINT for treating acute liver failure, inflammation,  
 PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic  
 PT and proinflammatory activity  
 XX  
 XX Claim 30; Fig 1; 99pp; English.

The present invention describes therapeutic applications of mature FLINT  
 CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT  
 CC (mFLINT), which is a member of the tumour necrosis factor receptor  
 CC superfamily, is used for treating acute liver failure, inflammation of  
 CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated  
 CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated  
 CC injury or disorder such as hypercoagulation (including use with  
 CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury  
 CC or disorder, Type I diabetes, cancer, cell damage or damage to an  
 CC innocent bystander tissue that is induced by a chemotherapeutic agent or  
 CC therapeutic irradiation, treating haematopoietic progenitor cells that  
 CC have been exposed to therapeutic radiation or chemotherapy, aplastic  
 CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is  
 CC also used for promoting the growth or differentiation of a haematopoietic  
 CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte  
 CC resulting from abnormal myocardial ischaemia. The present sequence  
 CC represents human FLINT.  
 XX  
 XX Sequence 300 AA:  
 SQ

Query Match 100.0%; Score 1634; DB 20; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 5,8e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MRLAEGPGLSLICLVLPALPVPAYRGVAETPTYPMPDAGTGRVYACCPGETVQR 60
Db 1 mralaegpgslslclvlpalpvpayrgvaetpypmrdagtgtrvyaacqpgpqlvqr 60
QY 61 PCRDSPTTGCPGPPRHNTQFWMYLERCRVCNVLGSEEREERACHATHNRACRRTGFF 120
Db 61 pcrdspttcgpcpprhntqfwmylecrvcnvlgeereearachathnaccrtgff 120
QY 121 AHAGFCLHASCPPGAGVIAPGTPSONTCQPCPGTFSASSSSSEOCQPHRNCTALGLA 180
Db 121 ahagfclhascppgagviapgtpsontcqpccpgtfsasssseocqphnctaigla 180
QY 181 LNVPGSSHDITLCTSGTFEPPLSTRVPAECCERAVIDFAFODISIKRLQRLQALBAPE 240
Db 181 lnvpgsshdltctscgtfpplstrvpaeecceravidfafigdisikrlqlqaleape 240
QY 241 GMPPTPRAGRAALQKLRRRLTELLGAODGALLVRLQALRYARMPGLERSVREERFLPVH 300
Db 241 gmpptpragraalqklrrrltellgaodgallvrlqalryarmpglersvreflrvh 300

RESULT 5
AA17479
ID AA17479 standard; Protein; 300 AA.
XX
AC AA17479;
XX
DT 02-AUG-1999 (first entry)
XX
DE Mammalian tumour necrosis factor receptor OPG-2.
XX
KM Tumour necrosis factor receptor; TNF receptor; OPG-2; Paget's disease;
KM osteopenic disorder; osteoclast activity; primary osteoporosis;
KM hyperglycemia; osteolytic metastasis; immune response; cancer.
XX
OS Mammalia.
XX
PN WO9926977-A1.
XX
PD 03-JUN-1999.
XX
PF 24-NOV-1998; 98WO-US25065.
XX
PR 17-FEB-1998; 98US-0074896.
PR 24-NOV-1997; 97US-0066446.
XX
PA (BIOJ ) BIOGEN INC.
XX
PI Tschoopp J.
XX
DR WPI: 1999-347693/29.
DR N-PSDB: AAX76052.
XX
PT New tumour necrosis factor family receptor OPG-2
PS Claim 1; Page 18; 22pp: English.
XX
XX The present sequence represents a mammalian tumour necrosis factor
XX receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis
XX factor receptor family, and can be used: (i) to raise specific
XX antibodies (Ab), (ii) to treat osteopenic disorders associated with
XX excessive osteoclast activity, e.g. primary osteoporosis, Paget's
XX disease, hyperglycaemia of malignancy, or osteolytic metastases; (iii)
XX for affinity purification of cognate ligands, and (iv) to screen for
XX ligands (antagonists or agonists). Ab, or other OPG-2 blocking agents
XX such as soluble forms of the protein, are used to prevent, or reduce
XX severity of, an immune response, and for treating cancer. They can also
XX be used in diagnostic assays. The nucleic acid sequence encoding OPG-2
XX can be used as a probe to isolate related sequences from other species.
XX
XX Sequence 300 AA:

```

```

Query Match 100.0%; Score 1634; DB 20; Length 300;
Best Local Similarity 100.0%; Fred. No. 5.8e-122;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLAEGPGLSLICLVLPALPVPAYRGVAETPTYPMPDAGTGRVYACCPGETVQR 60
Db 1 mralaegpgslslclvlpalpvpayrgvaetpypmrdagtgtrvyaacqpgpqlvqr 60
QY 61 PCRDSPTTGCPGPPRHNTQFWMYLERCRVCNVLGSEEREERACHATHNRACRRTGFF 120
Db 61 pcrdspttcgpcpprhntqfwmylecrvcnvlgeereearachathnaccrtgff 120
QY 121 AHAGFCLHASCPPGAGVIAPGTPSONTCQPCPGTFSASSSSSEOCQPHRNCTALGLA 180
Db 121 ahagfclhascppgagviapgtpsontcqpccpgtfsasssseocqphnctaigla 180
QY 181 LNVPGSSHDITLCTSGTFEPPLSTRVPAECCERAVIDFAFODISIKRLQRLQALBAPE 240
Db 181 lnvpgsshdltctscgtfpplstrvpaeecceravidfafigdisikrlqlqaleape 240
QY 241 GMPPTPRAGRAALQKLRRRLTELLGAODGALLVRLQALRYARMPGLERSVREERFLPVH 300
Db 241 gmpptpragraalqklrrrltellgaodgallvrlqalryarmpglersvreflrvh 300

RESULT 6
AA106817
ID AA106817 standard; Protein; 300 AA.
XX
AC AA106817;
XX
DT 24-JUN-1999 (first entry)
XX
DE Human DCR3 polypeptide.
XX
KM DCR3 polypeptide; tumour necrosis factor receptor; TNFR; Fas ligand;
KM apoptosis; T cell mediated immune response; allergy; asthma; cancer;
KM rheumatoid arthritis; Crohn's disease; guest vs. host disease; human;
XX gene therapy.
XX
OS Homo sapiens.
XX
PN WO9914330-A1.
XX
PD 25-MAR-1999.
XX
PF 18-SEP-1998; 98WO-US19661.
XX
PR 30-JUL-1998; 98US-0094640.
PR 18-SEP-1997; 97US-0059288.
XX
PA (GERTH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Botstein D, Dodge KH, Goddard A, Gurney AL;
PI Kim KJ, Lawrence DA, Pilti R, Roy MA, Tumas DB;
PI Wood WI;
XX WPI: 1999-244032/20.
XX N-PSDB: AAX32744.
XX
PT DCR3 polypeptide related to tumor necrosis factor receptor
PS Claim 5; Fig 1; 88pp: English.
XX
XX This represents a human DCR3 polypeptide, a homologue of tumour necrosis
XX factor receptor (TNFR) polypeptide. Host cells containing a vector
XX expressing the DCR3 nucleic acid can be used for the recombinant
XX production of the protein. DCR3 binds to Fas ligand, so it (or its
XX chimera) are useful for modulating apoptosis in mammalian cells, also
XX other Fas-ligand induced activities, particularly to inhibit T cell
XX mediated immune responses, e.g. in treatment of allergy, asthma,
XX rheumatoid arthritis, Crohn's disease, guest vs. host disease etc. DCR3

```



XX HUMAN NTR-1; orphan receptor; osteoprotegerin; OPB; TNFR; human;  
 KW tumour necrosis factor receptor; muscle disorder; bone mass; screening;  
 KM muscle metabolism; binding agent; cognate ligand.  
 XX Homo sapiens.  
 OS  
 XX WO9907738-A2.  
 PN  
 XX 18-FEB-1999.  
 PD  
 XX 04-AUG-1998; 98WO-US16202.  
 PF  
 XX 06-AUG-1997; 97US-0054869.  
 PR  
 XX (PROC.) PROCTER & GAMBLE CO.  
 PA (REGE-) REGENERON PHARM INC.  
 XX Maslakowski PJ, Morris J, Valenzuela DM;  
 PI WPI: 1999-167365/14.  
 DR N-PSDB; AAX23300.  
 XX  
 PT Novel orphan human receptor polypeptide and nucleic acid - useful as  
 PT diagnostic reagents and for treatment of muscle disorders  
 XX  
 PS Claim 7; Page 21; 23pp; English.  
 CC This represents a HUMAN NTR-1 polypeptide, a novel orphan receptor. The  
 CC protein is related to osteoprotegerin (OPB) and to tumour necrosis factor  
 CC receptor (TNFR). Host cells transformed with a vector comprising the  
 CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the  
 CC protein. HUMAN NTR-1 proteins and antibodies immuno specific for the  
 CC protein are useful for diagnosis and treatment of humans and animals,  
 CC especially muscle disorders, as the receptor is involved in regulation of  
 CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful  
 CC for screening for novel binding agents, and cognate ligands, which may be  
 CC used to treat disorders associated with HUMAN NTR-1 imbalance.  
 CC  
 SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 20; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRALEGPGLSILCLVLAIPALPALLVPVAVRGVAETPTYPWRDAETGSRILVCAQCPPTGFVOR 60  
 DB 1 mralepgpilsilclvialpalilpvpavrgvaeetpypwrdaetgerlvcaqcpptgtvr 60  
 OY 61 PCRRDSPPTGCPPPRHHTQFMWYLERCRYCNVLCGEREEERACHATNHRACRCRTGFF 120  
 DB 61 pcrdspttcgpcpprhytqfwmyletercyenlgerereearachathnraactrtgff 120  
 OY 121 AAHAGFCLHASCPRGAGVIAPGTPSONTOCPCPGTSSASSSSSECCOPHRNCTALGLA 180  
 DB 121 ahagfclhascprgagviapgtspntcpcpgtssassssseccqphnrcatgl 180  
 OY 181 LNVPGSSSHDPLCTSCGPFPLSTRVPGAECEERAVIDFAVADODISIKRLORLQALAEAP 240  
 DB 181 lnvpgssshdplctscgpfplstrvpgaeceeravidfaadodisikrlqlqaleape 240  
 OY 241 GWCPTPAGRAAIQALKIRRLTELGAQDQALLVRLQALRVARNPCLERSVRERELPHY 300  
 DB 241 gwcptraagaaqlkirlrtellgaqdalvlvrlqalrvarnpclersverrelphv 300

RESULT 9  
 AABI9335  
 ID AABI9335 standard; Protein; 300 AA.  
 XX AABI9335;  
 AC  
 XX

DT 19-FEB-2001 (first entry)  
 DE A full length human FAS ligand Inhibitory Protein (FLINT).  
 XX  
 XX Human; FAS ligand Inhibitory Protein; FLINT; analogue; apoptosis;  
 KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;  
 KM acute respiratory distress syndrome; ulcerative colitis;  
 XX chronic obstructive pulmonary disease; Crohn's disease.  
 XX Homo sapiens.  
 OS  
 XX WO200058465-A2.  
 PN  
 PD 05-OCT-2000.  
 XX  
 XX 20-MAR-2000; 2000WO-US06417.  
 PF  
 XX 30-MAR-1999; 99US-0126839.  
 PR 21-JUN-1999; 99US-0140077.  
 PR 21-JUN-1999; 99US-0140156.  
 PR 20-OCT-1999; 99US-0160566.  
 PR 18-FEB-2000; 2000US-0183398.  
 XX  
 PA (ELIL) LILLY & CO ELI.  
 PI Becker GW, Cohen FJ, Gonzalez-dewhilt PA, Hale JE, Micanovic R;  
 PI Newton CM, Nobilit TW, Natimachalam R, Tschang SR, Wiltcher DR;  
 PI Wroblewski VJ.  
 DR WPI: 2000-656167/63.  
 XX  
 PT FAS ligand Inhibitory Protein analogs useful for treating abnormal  
 PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,  
 PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's  
 PT disease -  
 PS Disclosure: Page 113-114; 114pp; English.  
 XX  
 XX The present sequence represents a full length human FAS ligand Inhibitory  
 CC Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor  
 CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature  
 CC FLINT protein is modified to produce analogues, which have greater  
 CC potency, longer in vivo half-lives, decreased aggregation, decreased  
 CC absorption onto surfaces, increased solubility and improved ease of  
 CC formulation. The FLINT analogue is useful for treating a patient  
 CC suffering from disease or condition relating to abnormal apoptosis such  
 CC as acute lung injury, acute respiratory distress syndrome, pulmonary  
 CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or  
 CC Crohn's disease.  
 CC  
 SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRALEGPGLSILCLVLAIPALPALLVPVAVRGVAETPTYPWRDAETGSRILVCAQCPPTGFVOR 60  
 DB 1 mralepgpilsilclvialpalilpvpavrgvaeetpypwrdaetgerlvcaqcpptgtvr 60  
 OY 61 PCRRDSPPTGCPPPRHHTQFMWYLERCRYCNVLCGEREEERACHATNHRACRCRTGFF 120  
 DB 61 pcrdspttcgpcpprhytqfwmyletercyenlgerereearachathnraactrtgff 120  
 OY 121 AAHAGFCLHASCPRGAGVIAPGTPSONTOCPCPGTSSASSSSSECCOPHRNCTALGLA 180  
 DB 121 ahagfclhascprgagviapgtspntcpcpgtssassssseccqphnrcatgl 180  
 OY 181 LNVPGSSSHDPLCTSCGPFPLSTRVPGAECEERAVIDFAVADODISIKRLORLQALAEAP 240  
 DB 181 lnvpgssshdplctscgpfplstrvpgaeceeravidfaadodisikrlqlqaleape 240



QY 241 GNGPTPRAGRAALQKLRRLTELLGAQDALLVRLQLARVARMPGLERSVERFLPVH 300  
 DB 241 gwgpptpragraalqklrrrlteligagdgallvrlqlarvarmpglersverflpvh 300

RESULT 10  
 AAB28559  
 ID AAB28559 standard; protein; 300 AA.  
 AC AAB28559;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX

DE Human soluble TNF receptor tnfrsf-1.  
 XX  
 KW Human: tumour necrosis factor like-1; TNF1; tumour necrosis factor; TNF;  
 KW immunosuppressive; antihistaminic; neuroprotective; dermatological;  
 KW antiinflammatory; antidiabetic; cytosolic; osteoprotic; gene therapy;  
 KW colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;  
 KW osteoporosis; autoimmune disease; myasthenia gravis;  
 KW insulin-dependent diabetes mellitus.

XX Homo sapiens.  
 XX MO200060079-A2.  
 XX  
 PD 12-OCT-2000.  
 PF 05-APR-2000; 2000MO-US09058.  
 XX  
 PR 05-APR-1999; 99US-0286529.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX

PI Tribouley C;  
 PI  
 DR WPI: 2000-665004/64.  
 DR N-PSDB: AAC63764.

PT Tumour necrosis factor (TNF) and TNF receptor superfamily protein  
 PT members TNF-L and TNFR-L, useful for enhancing or decreasing TNF  
 PT activities such as inducing cell death and lymphoid organogenesis -  
 XX  
 PS Claim 1: Page 72; 77pp; English.

XX The present sequence is given in a specification relating to an isolated  
 CC human protein designated tumour necrosis factor like-1 (TNFL1). It may be  
 CC used to induce cell death in tumours, to induce apoptosis of activated T  
 CC cells, to induce inflammation, and to rescue resting T cells from  
 CC apoptosis. TNF receptors are used to regulate the function of a TNF  
 CC ligand which plays a role in apoptosis, inflammation, differentiation, or  
 CC proliferation. Expression of the receptors can also be useful as markers  
 CC for cancer, especially for colon cancer. Diseases which can be treated  
 CC using ligands and/or receptors of the TNF/TNFR superfamily include  
 CC rheumatoid arthritis, cancer, septic shock, Crohn's disease and  
 CC osteoporosis. The polynucleotides can be used in gene delivery vehicles,  
 CC for the purpose of delivering a mRNA or oligonucleotide, full-length  
 CC protein, fusion protein, polypeptide, or ribozyme, or single-chain  
 CC antibody, into a cell. The newly identified receptor proteins play  
 CC regulatory roles in cell proliferation and/or differentiation. The  
 CC receptors can also play a role in the negative regulation of  
 CC osteoclastogenesis. Soluble TNFR-like receptors can be useful in the  
 CC neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be  
 CC used to treat autoimmune diseases (myasthenia gravis and  
 CC insulin-dependent diabetes mellitus), tumours, and proliferative  
 CC disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be  
 CC delivered to subjects for the purpose of screening test compounds for  
 CC those which are useful for enhancing transfer of TNF-L subgenomic  
 CC polynucleotides to the cell or for enhancing subsequent biological  
 CC effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.  
 XX  
 XX Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 5,8e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALGPGSLILCLIVLALPALLVPVPAVRGVAETPTVPMRAEGERLYVCACQCPPTFVOR 60  
 DB 1 mralgpgslilclivlalpallvpvparvgaetpvtvpmraegetvlyvcacqcpptfvtqr 60  
 QY 61 PCRDSPTTCGPPRRHYTFYFMVYLERCRCNVLCGEEREERACNATHRACRCRTGFF 120  
 DB 61 pcrdspttcgpprrhytfyfmylercrcnvlcgeereeracnathracrcrtgff 120  
 QY 121 AHAGFCLHNASCPGAGVIAPGTPSQNTQCPQPPPTFSASSSSSECCQPHRNCTALGLA 180  
 DB 121 ahagfclhnascpagviapgtpsqntqcpqppptfsassssseqcphrncalglia 180  
 QY 181 LNPVSSSHHTLTCTSCGFLSTRVGAEECECAVINDFAFQDSTIKRLQALALEAPE 240  
 DB 181 lnpvssshhtlctscgflstrvgaeececaavidfvafigdlsikrllqaleape 240  
 QY 241 GNGPTPRAGRAALQKLRRLTELLGAQDALLVRLQLARVARMPGLERSVERFLPVH 300  
 DB 241 gwgpptpragraalqklrrrlteligagdgallvrlqlarvarmpglersverflpvh 300

RESULT 11  
 AAB24057  
 ID AAB24057 standard; protein; 300 AA.  
 AC AAB24057;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX

DE Human PRO212 protein sequence SEQ ID NO:2.  
 XX  
 KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 KW proliferation; tumorigenesis; identification; cancer; cytostatic;  
 KW neurotropic; neuroprotective; antiinflammatory; immunosuppressive;  
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
 KW neuronal disorder; glioma disorder; astrocytoma disorder; angiogenic;  
 KW hypothalamic disorder; glandular disorder; macrophage disorder;  
 KW epithelial disorder; stromal disorder; blastocytic disorder;  
 KW inflammatory disorder; immunologic disorder.  
 XX

OS Homo sapiens.  
 XX  
 PN MO200053755-A2.  
 XX  
 PD 14-SEP-2000.  
 PF 06-JAN-2000; 2000MO-US00376.  
 XX  
 PR 08-MAR-1999; 99MO-US05028.  
 PR 02-JUN-1999; 99MO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 30-NOV-1999; 99MO-US28313.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 05-JAN-2000; 2000MO-US00219.  
 XX  
 PA (GENET ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA,  
 PI Watanabe CK, Wood WI;  
 XX  
 DR WPI: 2000-572270/53.  
 DR N-PSDB: AAC58367.  
 XX  
 PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 PT treatment, diagnosis and prevention of cancer -  
 XX

PS Claim 61; Fig 2; 286pp; English

The present invention describes an isolated antibody that binds to CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR PRO2188. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds may be used to treat various conditions, including those characterised by overexpression and/or activation of the amplified CC PRO genes. Exemplary conditions or disorders for which treatment with such CC antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours), CC leukemias and lymphoid malignancies, other disorders such as neuronal, CC glial, astrocytal, hypothalamic and other disorders, macrophagal, CC epithelial, stromal and blastocoele disorders, and inflammatory, CC angiogenic and immunologic disorders. Acc58242, to Acc58366 represent PCR CC primers and hybridisation probes used in the isolation of the human PRO CC sequences. Acc58367 to Acc58396 and AAB24057 to AAB24089 represent human CC PRO polynucleotide and protein sequences given in the exemplification of CC the present invention.

Sequence	300 AA
SQ	

Query Match	100.0%;	Score 1634;	DB 21;	Length 300;
Best Local Similarity	100.0%;	Pred. No. 5.8e-122;		
Matches 300; Conservative	0;	Mismatches	0;	Gaps 0

QY	1	MRALBERGSLTCLVIALVLPALLPVPAYKGAVENTPTYPMDADATGRLVACACPGSTVOR	60
Dp	1	mralbergsltsclviallpallpvparygaventptypmdaetgerlvacqpgstfvtgr	60
QY	61	PCRDRSPMTCGCGPRRHTTQWNTLBCRCXCNVLGSEEREERAAATHNNACRCRIGFF	120
Dp	61	pcrrdrspmcgcprrhnytdqkwnylbcrcxcmnlgsereearacathnmacrcrgrgfl	120
QY	121	AHAAGFLEHASCPCGAGVIAIAPGTPSONTQCPCPCPGTSSASSSSSEDCQPHRNCYALGLA	180
Dp	121	ahagficlehascpaagviapagtpsqntqpcpgppltsassssseqdqpnmntalgla	180
QY	181	LNVPGSSSHDTLCTSCCTGFPSTRVPGAEBCERAVIDFAAFDIDISIKRLQILQALEAPE	240
Dp	181	lnvpgssshdtlctactctfplstrvpaeececravidfaifdaisikrlqflqaleape	240
QY	241	GMPPTFRACARALQQLKRRRIITTELIGADODALVLRLLQALIRARMPGCLERSVRRERFLPVH	300
Dp	241	gmppptfracraalqklrrrtitelllqgdqallvlllqalirampglsrsvrrerflpvh	300

## RESULT 12

ID AAB33416 standard; Protein; 300 AA

AC AAB33416;

DT 29-JAN-2001 (first entry)

DE Human PRO212 protein UNQ186 SEQ ID NO:14

KM Human: immune related disease; diagnosis; antiinflammatory; cardanti;  
KM dermatological; antithyroid; antirheumatic; immunosuppressive;  
KM haemostatic; antithyroid; antidiabetic; neurotropic; neuroprotective;  
KM antineuritic; hepatotropic; virucide; antiparasitic; antileptic;  
KM antistaphylococcal; systemic lupus erythematosus; rheumatoid arthritis;  
KM osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
KM idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KM systemic vasculitis; autoimmune hemolytic anemia; diabetes mellitus;  
KM autoimmune thrombocytopenia; immune-mediated renal disease;

KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease.

OS Homo sapiens.

PN W0200053758-A2

PD 14-SEP-2000.

PF 02-MAR-2000; 2000WO-US05841.

PR	18-MAR-1999	99NOV-05050502
PR	10-MAR-1999	99NOV-01236318
PR	12-MAR-1999	99NOV-01239557
PR	23-MAR-1999	99NOV-01257577
PR	12-APR-1999	99NOV-01286843
PR	20-APR-1999	99NOV-03098615
PR	28-APR-1999	99NOV-03164435
PR	14-MAY-1999	99NOV-01325721
PR	14-MAY-1999	99NOV-01344877
PR	22-JUN-1999	99NOV-05112552
PR	20-JUN-1999	99NOV-01410357
PR	20-JUL-1999	99NOV-01441598
PR	28-JUL-1999	99NOV-01456599
PR	01-SEP-1999	99NOV-05201122
PR	08-SEP-1999	99NOV-05201122
PR	13-SEP-1999	99NOV-05205954
PR	15-SEP-1999	99NOV-05210940
PR	15-SEP-1999	99NOV-05212497
PR	05-OCT-1999	99NOV-05233089
PR	29-OCT-1999	99NOV-01626306
PR	29-NOV-1999	99NOV-05282813
PR	30-NOV-1999	99NOV-05282814
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PR	16-DEC-1999	99NOV-05300955
PR	20-DEC-1999	99NOV-05309999
PR	30-DEC-1999	99NOV-05313174
PR	05-JAN-2000	2000NOV-05302193
PR	06-JAN-2000	2000NOV-05302777
PR	06-JAN-2000	2000NOV-05303777
PR	11-FEB-2000	2000NOV-05303655
PR	18-FEB-2000	2000NOV-05304341
PR	18-FEB-2000	2000NOV-05304442
PR	22-FEB-2000	2000NOV-05304414

PA (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W  
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
PT immune related disorders, e.g. systemic lupus erythematosus, Rheumatoid  
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
XX  
Claim 33; Fig 6; 30pp; English.  
SS

CC The present invention describes sixty four human PRO proteins which can  
CC be used in the treatment of immune related diseases. The human PRO  
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
CC treating and diagnosing immune related disorders. The disorders are

CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
CC autoimmune or immune-mediated skin diseases, allergic diseases,  
CC immunological diseases of the lung, and transplantation associated  
CC diseases including graft rejection and graft-versus-host-disease.  
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
CC AAB3414 to AAB3477 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
XX

Sequence 300 AA:

Query Match 100.0%; Score 1634; DB 21; Length 300;  
Best Local Similarity 100.0%; Pred. No. 5,8e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRALBGPGLSLCLVLALPALLPVPAVRGVAETPTYPWMDAETGERLYVCAQCPTGTFVQR 60  
DB 1 mralebgpgslslclvlalpallvpavrgvaeelptypwdaetgerlyvcacqcpptgtvqr 60  
OY PCRBDSTTCGPPCPRHYYQFMWYLERCRVCNVLGGEREEAACHATHRARCRRTGFF 120  
DB 61 pcrbdsttcgppcprhyqfmylercrycnvlgereeeaaachathrarcrctgff 120  
OY 121 AHAGFCLAEHASCPPGAGVIAVPGPSONTQCPCPPGTFSSASSSSSECCQPHRCTALGIA 180  
DB 121 ahagfclenascpvgavilavpgpsontgcqppgtfssassssseqcqhrcntalgi 180  
OY 181 LNPVGSSSHDTLCTSCGPFPLSTRVPGAECEBAVIDEFAFODISIKRIQLQALEAPE 240  
DB 181 lnpvgssshdtlctscgtgfpflstrvpgaeceavidfafqdisikrlqilqaleape 240  
OY 241 GMSGPTPRAGRAALQIKLRRLTELGAQDALLVRLQALRVARMGLESVREERLPVH 300  
DB 241 gmsgptpragraalqiklrrrltelgagdgallvrlqalrvarmglsvererflpvh 300

RESULT 13

AAB03621  
ID AAB03621 standard; Protein; 300 AA.

XX  
AC AAB03621;

XX  
DT 03-JAN-2001 (first entry)

XX  
DE Human Fas ligand inhibitor FLINT.

XX  
KW Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;  
KW inflammation; infectious disease; ischaemia; Alzheimer's disease;  
KW Parkinson's disease; Crohn's disease; transplantation.

XX  
OS Homo sapiens.

XX  
FH key Location/Qualifiers

FT Peptide 1..29 /label= signal\_peptide

FT Protein 30..300 /label= mature\_FLINT

FT Domain 1..42 /label= domain\_1

FT Domain 43..85 /label= domain\_2

FT Domain 86..122 /label= domain\_3

FT Domain 123..165 /label= domain\_4

FT

XX  
PN MO200034782-A1.

XX  
PD 15-JUN-2000.

XX  
PF 07-DEC-1999; 99MO-US28696.

XX  
PR 09-DEC-1998; 98US-0111575.

XX  
PR 09-DEC-1998; 98US-0111580.

XX  
PR 07-JAN-1999; 99US-0115069.

XX  
PA (ELIL ) LILLY & CO ELI.

XX  
PI Rosteck PRJ, Song HY, Su EW;

XX  
DR N-PSDB; AAA53208.

XX  
PT Novel monkey Fas ligand inhibitor polypeptides, useful for treating

XX  
PT inflammatory or autoimmune disease such as rheumatoid arthritis,

XX  
PT infectious diseases such as chronic hepatitis, and

XX  
PT Ischaemia/Re-perfusion conditions -

XX  
PS Claim 19; Page 91-93; 101pp; English.

CC The present sequence is the protein sequence of the human Fas ligand  
CC inhibitor (FLINT). The FLINT protein is involved in cell-specific  
CC apoptosis, and can be used to treat inflammatory and autoimmune diseases  
CC such as rheumatoid arthritis, inflammatory bowel disease,  
CC graft-versus-host disease, diabetes, psoriasis and Graves' disease,  
CC infectious diseases such as HIV-induced lymphopenia, fulminant viral  
CC hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated  
CC mucocardial infarction, acute coronary syndrome, congestive heart failure  
CC and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung  
CC injury and acute respiratory distress syndrome, Crohn's disease, brain  
CC trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic  
CC anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and  
CC multiple sclerosis. In addition, the protein and its gene can be used to  
CC prevent apoptosis following organ transplantation.

XX  
SQ Sequence 300 AA:

Query Match 100.0%; Score 1634; DB 21; Length 300;  
Best Local Similarity 100.0%; Pred. No. 5,8e-122;

Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRALBGPGLSLCLVLALPALLPVPAVRGVAETPTYPWMDAETGERLYVCAQCPTGTFVQR 60

DB 1 mralebgpgslslclvlalpallvpavrgvaeelptypwdaetgerlyvcacqcpptgtvqr 60

OY 61 PCRBDSTTCGPPCPRHYYQFMWYLERCRVCNVLGGEREEAACHATHRARCRRTGFF 120

DB 61 pcrbdsttcgppcprhyqfmylercrycnvlgereeeaaachathrarcrctgff 120

OY 121 AHAGFCLAEHASCPPGAGVIAVPGPSONTQCPCPPGTFSSASSSSSECCQPHRCTALGIA 180

DB 121 ahagfclenascpvgavilavpgpsontgcqppgtfssassssseqcqhrcntalgi 180

OY 181 LNPVGSSSHDTLCTSCGPFPLSTRVPGAECEBAVIDEFAFODISIKRIQLQALEAPE 240

DB 181 lnpvgssshdtlctscgtgfpflstrvpgaeceavidfafqdisikrlqilqaleape 240

OY 241 GMSGPTPRAGRAALQIKLRRLTELGAQDALLVRLQALRVARMGLESVREERLPVH 300

DB 241 gmsgptpragraalqiklrrrltelgagdgallvrlqalrvarmglsvererflpvh 300

RESULT 14

AA97246  
ID AA97246 standard; Protein; 300 AA.

XX

AC AA97246;  
XX  
DT 19-DEC-2000 (first entry)  
DE M68 TNF receptor related protein.  
XX  
KW M68: tumour necrosis factor; TNF; programmed cell death; apoptosis;  
KW receptor; immune response; cell differentiation; ligand; cancer;  
KW bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;  
KW Grave's disease; idiopathic myxedema; autoimmune diabetes;  
KW thrombotic thrombocytopenic purpura; multiple sclerosis;  
KW liver diseases; autoimmune gastritis; ulcerative colitis;  
KW glomerulonephritis; pulmonary fibrosis; heart failure;  
KW atherosclerosis; aplastic anaemia; myelodysplastic syndromes;  
KW osteoporosis; Alzheimer's disease; Parkinsons disease; stroke;  
KW myocardial infarction; human.  
XX  
OS Homo sapiens.  
XX  
PN WO20046247-A1.  
XX  
PD 10-AUG-2000.  
XX  
PF 04-FEB-2000; 2000WO-US03037.  
XX  
PR 05-FEB-1999; 99US-0118902.  
PR 20-DEC-1999; 99US-0172754.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Bai C;  
XX  
DR WPI: 2000-506066/45.  
DR N-PSDB: AAA53800, AAA53801, AAA53802.  
XX  
PT Isolated human M68 nucleic acids and proteins which are part of the  
PT tumour necrosis factor receptor (TNFR) family, useful for identifying  
PT modulators that may be used to treat various diseases e.g. cancer,  
PT osteoporosis, Alzheimer's disease  
XX  
PS Claim 1: Page 75-76; 80pp; English.  
XX  
CC The M68 protein is a member of a family of proteins which have  
CC roles in immune responses, cell death, cell proliferation and  
CC stimulation of cell differentiation. M68 lacks a transmembrane domain  
CC and is a secreted factor suggesting that it functions as a natural  
CC inhibitor for its ligand. The altered expression pattern of M68 in a  
CC multitude of tissues suggests that M68 may play a role in cancer by  
CC binding to its ligand and blocking apoptotic cell death induced by  
CC such a ligand. This anti-apoptotic role of M68 suggests that  
CC modulators of M68 will be useful in treatment of apoptosis-related  
CC diseases such as various forms of cancer and various bone disorders.  
CC M68 nucleic acids and proteins are therefore useful for treating  
CC conditions involving atypical apoptosis and for identifying  
CC modulators of M68. Modulators of M68 are useful for treatment of  
CC cancer and other diseases associated with abnormal levels of  
CC apoptosis including systemic lupus erythematosus, Hashimoto's  
CC thyroiditis, Grave's disease, idiopathic myxedema, autoimmune  
CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,  
CC liver diseases, autoimmune gastritis, ulcerative colitis,  
CC glomerulonephritis, pulmonary fibrosis, heart failure,  
CC atherosclerosis, aplastic anaemia, myelodysplastic syndromes,  
CC osteoporosis, Alzheimer's disease, Parkinsons disease, stroke, and  
CC myocardial infarction.  
XX  
SO Sequence 300 AA:

Query Match 100.0%; Score 1634; DB 21; Length 300;  
Best Local Similarity 100.0%; Pred. No. 5,8e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRALEGGSLICLVIALPALPVPVAVRGVATPPYPRDAETGERLVCACQCPPTFFVOR 60

|||||  
Db 1 mraleppgisllcivlalpalpvpavrgvaeepcywdaetgerlvcagcpptffvr 60  
QY PCRDSPTTCGFCPPRHRYTOFWNYLERCRCNVLCGEEEREARACHATHNACGRCGFE 120  
Db 61 pcrdspttcgfcpprhytqfmylercrycnlcegeereaarachathnacrcrtgff 120  
QY 121 AHAGFLEHASCPPAGVYIAPGTPSQWTCOCPCPPTFSASSSSSEOCQPHRNTATGLA 180  
Db 121 ahagfclehascpagvayiapgtpsqwtqpcppptfssaasssseqcpbrnctalgla 180  
QY 181 LNVPGSSSHDTLCSTCGFPLSTFRVPGAECEERAVIDFAFODISIKRLOALQALFAPE 240  
Db 181 lnvpgssshdtlcsctcgfpstfrvpgaeceeravidfafgdisikrlqlqaleape 240  
QY 241 GWGPTPRAGRAALQKLRRLTELLAGODGALLVRLQALRYARMPGLERSVREPRIPVH 300  
Db 241 gwgpptpragraalqkrrrltellegdgallvrlqalryarmpglersvverfipvh 300

RESULT 15  
AA90357  
ID AA90357 standard; Protein: 300 AA.  
XX  
AC AA90357;  
XX  
DT 04-DEC-2000 (first entry)  
XX  
DE Human tumour necrosis factor receptor-6 alpha protein sequence.  
XX  
KE Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;  
KW ocular neovascularisation; solid tumour; malignancy; prostate cancer;  
KW breast cancer; colon cancer; diabetic retinopathy; microbial infection;  
KW pre-maturity macular degeneration; allergy; inflammation; tissue damage;  
KW thyroid associated ophthalmopathy; cell damage; parasitic infection;  
KW bone disease; osteoporosis; atherosclerosis; cardiovascular disease;  
KW neurodegenerative disorder; Alzheimer's disease; immune disorder;  
KW graft rejection; rheumatism; liver disease; autoimmune diabetes;  
KW psoriasis; septic shock; ulcerative colitis; therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200052028-A1.  
XX  
PD 08-SEP-2000.  
XX  
PF 03-MAR-2000; 2000WO-US05686.  
XX  
PR 04-MAR-1999; 99US-0121774.  
PR 12-MAR-1999; 99US-0124092.  
PR 27-APR-1999; 99US-0131279.  
PR 30-APR-1999; 99US-0131664.  
PR 02-AUG-1999; 99US-0146371.  
PR 01-DEC-1999; 99US-0168235.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Gentz RL, NI J, Ebner R, Yu G, Ruben SM, Feng P;  
XX  
DR WPI: 2000-572174/53.  
DR N-PSDB: AAA37772.  
XX  
PT Nucleic acids encoding human tumour necrosis factor receptor (TNFR)  
PT proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g.  
PT Alzheimer's disease, osteoporosis and graft rejection  
XX  
PS Claim 20; Fig 1; 332pp; English.  
XX  
CC This sequence represents the human tumour necrosis factor receptor 6  
CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA  
CC and protein sequences can be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate TNFR expression. The  
CC nucleic acids, polypeptides, antibodies, agonists and antagonists against

CC them may be used for the treatment of a range of conditions such as  
CC disorders associated with neovascularisation (especially ocular  
CC neovascularisation) (such as solid tumours and malignancies (e.g.  
CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy  
CC and pre-maturity macular degeneration), allergies, inflammation,  
CC thyroid associated ophthalmopathy tissue/cell damage, wounds, microbial  
CC and parasitic infections, bone disease (e.g. osteoporosis),  
CC atherosclerosis, pain, cardiovascular disease (e.g. stroke),  
CC neurodegenerative disorders (e.g. Alzheimer's disease), immune  
CC disorders (e.g. graft rejection), rheumatism, liver disease,  
CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative  
CC colitis.  
XX  
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;  
Best local Similarity 100.0%; Pred No. 5,8e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGPGLSLCLVIALPALPVPVAVRGVAETPTYPWMDAETGERLWCAQCPPTFVQR 60  
Db 1 mralepgjlsllclvialpallvpvavrgvaeptypwmdaetgerlwcacppgtftvqr 60  
QY 61 PCRDSPTTCGPPPPRHYTFWNYLERCRYCNVLCGEREBEARACHATNNRACRCRTGFF 120  
Db 61 pcrdspttcgpppprhytfwnylercrycnvlgereeeearachathnrcrcrtgff 120  
QY 121 AHAGFCLENHSCPPGAGVITAPGPPSONTOCOPPGTFSSSSSSFCOCOPHRMCTALGTA 180  
Db 121 ahagfclenhscppgagvitaipgspntcgcqppgtfssssssfcqphmctalglta 180  
QY 181 LNPSSSHDTLCTSGTFPLSTRVPGAEECEBAVIDFVAFODISIKRLQRLQALEAPE 240  
Db 181 lnpssshdtlctsgtfgflstrvpgaeecebaividfvafigdisikrlqrlqaleape 240  
QY 241 GWGPTPRAGRAALQIKURRRRLTELGAQDGALLVRLQALRVAMPGLERSVRERELPHV 300  
Db 241 gwgptpragraalqiklrrrltelllgaqdgallvrlqalrvampglersvrerelphv 300

Search completed: October 31, 2001, 12:38:44  
Job time: 358 sec

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303 ACCTGGAGCGCTGGCGCTACTGCAACGTCCTCTGGGGGAGCGTAGAG 352
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353 GAGGACAGCGGCTTGCCACAGCCACCAACCGTGGCTCCCGCTGGCGGAC 402
117 rGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysProp 134
403 CGGCTTCTTCGCGACGCTGGTTCTGCTTGAGAGCAGCATGCTGTCCAC 452
134 roGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCys 150
453 CTGGTCCCGCGGTGATTGCCCCGGGACCCCCAGCAGCAACAGCAGTGC 502
151 GlnProCysProproGlyThrPheSerAlaSerSerSerSerSerGluG1 167
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167 nCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValP 184
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653 CTCAGACACAGGTTACAGAGAGCTGAGAGTGTAGCGTCCCTCATGTGA 702
217 PheValAlaPheGlnAspIleSerIleLysArgLeuGlnArgLeuGlu 234
703 CTGTGTGCTTCCAGGACATCTCATCAAGAGGCTGCAGCGGCTGTGC 752
234 IlnAlaLeuGlnAlaProGluGlyThrGlyProThrProArgAlaGlyArg 250
753 AGGCCCTCGAGCCCGGAGGCGTGGGTCCGACACCAAGGGCGGCGCCG 802
251 AlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuGlyValI 267
803 GCGGCTTGCACGCTGAAGCTGCGTGGCGGCTCACGAGCTCTGGGGGC 852
267 aGlnAspGlyAlaLeuLeuValArgLeuGluGlnAlaLeuArgValAla 284
853 GCAGGAGCGGGCGGTGTGTGGGCTGTGAGGCGCTGCGCGGTGGCCA 902
284 rGlyMetProGlyLeuGlnArgSerValArgGluArgPheLeuProValHis 300
903 GGATGCCCGGGCTGGAGCGAGCGTCCGTGAGCGCTTCCCTGTGTGCAC 952

seq_name: gb_pat2:AX082868
seq_documentation_block:
LOCUS AX082868 1055 bp DNA PAT 28-FEB-2001
DEFINITION Sequence 1 from Patent W00110908.
ACCESSION AX082868
VERSION AX082868.1 GI:13184802
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Hsu, H.
TITLE Ntr3, a member of the tnf-receptor supergene family
JOURNAL Patent: WO 0110908-A1 15-FEB-2001;
Amgen Inc. (US)
FEATURES
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Location/Qualifiers
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/db_xref="GI:13184803"
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AUTHORS Ashkenazi, A.J., Goddard, A., Gurney, A.L., Hillan, K., Napier, M. and Wood, M.I.  
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Genentech, Inc. (US)  
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Godowski, P.J., Wood, W.I., Gurney, A.L., Hillan, K.J., Cohen, R.L.,  
Goddard, A.D., Botstein, D., and Ashkenazi, A.  
Genomic amplification of a decoy receptor for Fas ligand in lung  
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Nature 396 (6712), 699-703 (1998)  
JOURNAL  
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Sandig, V., Soderman, A., Galloway, S. M., Liu, Q., Austin, C. P. and
Caskey, C. T.
TITLE
Overexpression of M68/DCR3 in human gastrointestinal tract tumors
independent of gene amplification and its location in a four-gene
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JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
MEDLINE
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2 (bases 1 to 1428)
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Bailey, C.
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Direct Submission
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Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,
Summerytown Pike, West Point, PA 19403, USA
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 REFERENCE 1 (sites)  
 AUTHORS Kikuno,R., Nagase,T., Ishikawa,K., Hirose,M., Miyajima,N.,  
 Tanaka,A., Kotani,H., Nemura,N. and Ohara,O.  
 TITLE Prediction of the coding sequences of unidentified human genes.  
 XIV. The complete sequences of 100 new cDNA clones from brain which  
 code for large proteins in vitro  
 JOURNAL DNA Res. 6 (3), 197-205 (1999)  
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 REFERENCE 2 (bases 1 to 4228)  
 AUTHORS Ohara,O., Nagase,T. and Kikuno,R.  
 TITLE Direct Submission

JOURNAL Submitted (17-JUN-1999) to the DDBJ/EMBL/GenBank databases. Osamu  
 Ohara, Kazuo DNA Research Institute, Laboratory of DNA Technology;  
 Yama 1532-3, Kisarazu, Chiba 292-0812, Japan  
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ACCESSION AX093178  
VERSION AX093178.1 GI:13509626  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 936)  
AUTHORS Atkinson,P.R., Tian,Y. and Mitcher,D.R.  
TITLE Flint proteins and formulations thereof  
JOURNAL Patent: WO 0118041-A 3 15-MAR-2001;  
Eli Lilly AND COMPANY (US)  
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ACCESSION  AX097545
VERSION     AX097545.1  GI:13514210
KEYWORDS
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ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 936)
AUTHORS     Atkinson,P.R., Tian,Y. and Wlitcher,D.R.
TITLE       Plant analog compounds and formulations thereof
JOURNAL     Patent: WO 0118055-A 3 15-MAR-2001;
            Eli Lilly AND COMPANY (US)
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ACCESSION  AX098029
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ORGANISM    Homo sapiens
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REFERENCE   1 (bases 1 to 936)
AUTHORS     Atkinson,P.R., Tian,Y. and Wlitcher,D.R.
TITLE       Plant analog compounds and formulations thereof
JOURNAL     Patent: WO 0118202-A 3 15-MAR-2001;
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complete cds.
ACCESSION AF217796
VERSION AF217796.1 GI:7012928
KEYWORDS complete cds.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X.,
Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and
Caskey,C.T.
overexpression of M68/DCR3 in human gastro-intestinal tract tumors
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cluster
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
MEDLINE 20122600
PubMed 10655513
REFERENCE
AUTHORS Bai,C., Metzker,M.L., Liu,X. and Caskey,C.T.
DIRECT SUBMISSION
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LOCUS	Accession	Size	Species	Map	Date
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Human DNA sequence from clone RP4-583P15 on chromosome 20 contains ESTs, STRs, GSSs, and ten CpG islands. Contains the INR58b gene for tumor necrosis factor receptor 6b (decoy), the 3' part of the KIA1068 gene, the ARPP1 gene for ADP-ribosylation factor related protein 1, two genes for novel proteins, the gene for a G1074 enhancer factor and the gene for a novel zinc finger protein similar to rat RIN 2F and the gene for a novel BTF/POZ domain containing zinc finger protein, complete sequence.					

ACCESSION ALL21845  
VERSION GI:8246778  
KEYWORDS HTG; ADP-ribosylation factor; ANFRP1; BRB; CPG island; GLUT4 enhancer; KIAA1088; POZ; TNFRS6B; tumor necrosis factor; zinc finger.  
SOURCE human.

SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

**AUTHORS** Matthews, L.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (05-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire

COMMENT  
CB310 ISA, UK. E-mail enquiries: [humquery@sanger.ac.uk](mailto:humquery@sanger.ac.uk) Clone requests: [clonerequests@sanger.ac.uk](mailto:clonerequests@sanger.ac.uk)  
On Jun 4, 2000 this sequence version replaced gi:8052256.

COMMENT

During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Emu, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/Celegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20>

This sequence is the entire insert of clone RP4-583p15. The true left end of clone RP5-824A14 is at 27658 in this sequence. The right end of clone CPD-3184V7 is at 48631 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP4-583p15 is from the library RP01-4 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
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Mon Nov 5 08:22:40 2001

us-09-006-352-2.rge

Page 16

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OM of: US-09-006-352-2 to: N\_Geneseq\_0601: \* out\_format : pfs

Date: Oct 31, 2001 1:21 PM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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Query length: 300  
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KW apoptosis; inflammation; cancer; diabetes; acute liver failure;					
KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;					
KW reperfusion-associated injury; aplastic anaemia; differentiation;					
KW growth; myelodysplastic syndrome; pancytopenic condition;					
KW myocardial ischaemia; ss.					
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XX					
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PR 20-MAY-1998; 98US-0086074.					
PR 09-SEP-1998; 98US-0099643.					
PR 17-DEC-1998; 98US-0112577.					
PR 18-DEC-1998; 98US-0112703.					
PR 18-DEC-1998; 98US-0112933.					
PR 22-DEC-1998; 98US-0113407.					
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EA (ELIL ) LILLY & CO ELIL.					
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PI Bumo1 TF, Dou S, Glasbrook AL, Gould KE, Hale JE, Heuer JG;					
PI Hui KY, Khaitonenkov A, Mizrahi J, Na S, Nobilit TW, Reidy CA;					
PI Song HY, Wang J, Wu X, Zuckerman SH;					
DR WPI: 1999-591319/50.					
DR P-PSDB: AAZ2182.					
XX					
PT Use of mature FLINT for treating acute liver failure, inflammation,					
PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic					
PT and proinflammatory activity					
XX					
PS Claim 28; Fig 1; 99pp; English.					
XX					
The present invention describes therapeutic applications of mature FLINT					
(mFLINT) for use in the treatment of acute liver failure. Mature FLINT					
(mFLINT), which is a member of the tumour necrosis factor receptor of					
superfamily, is used for treating acute liver failure, inflammation of					
the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated					
with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated					
injury or disorder such as hypercoagulation (including use with					
thrombolytic or anti-thrombolytic agents), reperfusion-associated injury					
or disorder. Type I diabetes, cancer, cell damage or damage to an					
innocent bystander tissue that is induced by a chemotherapeutic agent or					
therapeutic irradiation, treating haematopoietic progenitor cells that					
have been exposed to therapeutic radiation or chemotherapy, aplastic					
anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is					
also used for promoting the growth or differentiation of a haematopoietic					
progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte					
resulting from abnormal myocardial ischaemia. The present sequence					
encodes human FLINT.					
XX					





























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601 GTGGCACCCACCGCAACTGCAGAGCCCTGGGCTGCTCAATGTGC 650
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701 CTCAGCACCAAGGATACAGAGCTGAGAGATGTGACGCTGCTCATCGA 750
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217 pPheValAlaPheGlnAspIleSerIleGlyArgLeuGlnArgLeuG 234
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XX anti allergic; antiasthmatic; immune related disorder;
XX hepato biliary disease; autoimmune disease; allergy; ss.
XX
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XX
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XX
XX 07-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-US15264.
XX
XX 02-JUN-1999; 99WO-US12252.
XX 20-JUL-1999; 99US-0144732.
XX 20-JUL-1999; 99US-0144758.
XX 28-JUL-1999; 99US-0146222.
XX 01-SEP-1999; 99WO-US20111.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 29-OCT-1999; 99US-0162506.
XX 30-NOV-1999; 99WO-US28313.
XX 01-DEC-1999; 99WO-US28634.
XX 09-DEC-1999; 99US-0170262.
XX 20-DEC-1999; 99WO-US30911.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.

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PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godwaski PJ, Gurney AL,
XX Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
XX Wood WI;
XX
XX WPI: 2001-025253/03.
XX P-PSDB; AAB50903.
XX
XX Thirtly three nucleic acids encoding PRO polypeptides which are useful
XX in the diagnosis and treatment of immune related disorders, e.g.
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX thyroiditis and diabetes mellitus -
XX
XX Claim 48; Fig 3; 218pp; English.
XX
XX The present sequence is one of thirty three nucleic acids encoding PRO
XX polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
XX antagonists are useful for treating and diagnosing immune related
XX disorders such as systemic lupus erythematosus, rheumatoid arthritis,
XX osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
XX syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
XX immune-mediated renal disease, demyelinating diseases of the central,
XX and peripheral nervous systems (such as multiple sclerosis, idiopathic
XX demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
XX inflammatory demyelinating polyneuropathy), hepatobiliary diseases
XX (such as infectious, autoimmune chronic active hepatitis, primary
XX biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
XX inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
XX disease, autoimmune or immune-mediated skin diseases (such as bullous
XX skin diseases, erythema multiforme, contact dermatitis, psoriasis),
XX allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
XX food hypersensitivity and urticaria), immunological diseases of the
XX CC lung (such as eosinophilic pneumonia), idiopathic pulmonary fibrosis
XX and hypersensitivity pneumonitis), transplantation associated diseases
XX including graft rejection and graft-versus-host diseases.
XX
XX SQ Sequence 1114 BP; 188 A; 379 C; 356 G; 191 T; 0 other;
XX
XX
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XX      Quality: 1634.00      Length: 300
XX      Ratio: 5.447      Gaps: 0
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XX 151 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 200
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 AC AAV07654;  
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 XX  
 XX 02-DEC-1998 (first entry)  
 XX  
 XX Nucleotide sequence of tumour necrosis related receptor (TR4).  
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 XX Human; tumour necrosis related receptor; TR4; agonist; antagonist;

KW Inhibition; chronic; acute; inflammation; arthritis; septicaemia;  
 KW autoimmune disease; transplant rejection; stroke; cancer;  
 KW Alzheimer's disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
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 FT /\*tag= a  
 FT /product= "human TR4"  
 XX  
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 XX  
 PD 02-SEP-1998.  
 XX  
 PE 20-JAN-1998; 98EP-0300382.  
 XX  
 PR 04-FEB-1997; 97US-0794796.  
 XX  
 PA (SMK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PT Emery J, Tan KB, Truneh A, Young PR;  
 PT WPI; 1998-508248/44.  
 DR P-PSDB; AAW66102.  
 XX  
 PT New DNA encoding tumour necrosis related receptor - used to treat  
 PT and prevent e.g. inflammation, arthritis, septicaemia, autoimmune  
 PT diseases, transplant rejection, infection, stroke, ischaemia, ARDS,  
 PT restenosis, AIDS, bone disorders and cancer  
 XX  
 PS Claim 3; Fig 1; 21pp; English.  
 XX  
 CC This is the nucleotide sequence of the human tumour necrosis related  
 CC receptor (TR4), used in the method of the invention. The TR4 protein  
 CC or its agonist can be used to treat a subject in need of enhanced  
 CC TR4 polypeptide activity. The antagonist is used to inhibit TR4  
 CC polypeptide activity. The active agents can be used for the  
 CC treatment and prevention of diseases such as chronic and acute  
 CC inflammation, arthritis, septicaemia, autoimmune diseases, transplant  
 CC rejection, stroke, cancer, Alzheimer's disease.  
 XX  
 SO Sequence 1164 BP; 206 A; 396 C; 355 G; 207 T; 0 other;  
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 161 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 210  
 34 rothrYrProTyrPArgAspAlaGlnThrGlyGlnArgLeuValAlaCysAla 50  
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 51 GlnCysProProGlyThrPheValGlnArgProCysArgArgAspSer 67  
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 67 othrThrCysGlyProCysProProArgHisTyrThrGlnPheTyrPant 84



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101 GluAlaArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgTh 117
|||||
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|||||
117 rGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysProp 134
|||||
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OM of: US-09-006-352-1 to: A\_Geneseq\_0601: \* out-format : pfs

Date: Oct 31, 2001 12:31 PM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

#### Command line parameters:

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KW: human; tumour necrosis related receptor; TR4; agonist; antagonist;

KW: inhibition; chronic; acute; inflammation; arthritis; septicemia;

KW: autoimmune disease; transplant rejection; stroke; cancer;

KW: Alzheimer's disease.

OS: Homo sapiens.

PN: P861850-A1.

PD: 02-SEP-1998.

PF: 20-JAN-1998; 98EP-0300382.

PR: 04-FEB-1997; 97US-0794796.

PA: (SWIK ) SMITHKLINE BEECHAM CORP.

PI: Emery J, Tan KB, Truneh A, Young PR;

DR: WPI; 1998-508248/44.

XX: N-PSDB; AAV07654.

PT: New DNA encoding tumour necrosis related receptor - used to treat

PT: and prevent e.g. inflammation, arthritis, septicemia, autoimmune

PT: diseases, transplant rejection, infection, stroke, ischaemia, ARDS,

PT: stenosis, AIDS, bone disorders and cancer

PS: (claim 1; Fig 1; 21pp; English.

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DE Human tumour necrosis factor receptor-6 alpha; TNFR-6 beta;
DE endothelial cells; keratinocytes; normal prostate; apoptosis;
DE prostate tumour tissue.
KW Homo sapiens.
KW OS
XX Key location/Qualifiers
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FT Protein 31..300
FT Note="TNFR-6 alpha"
FT Region 31..282
FT Note="Soluble extracellular domain"
XX W09830694-A2.
XX 16-JUL-1998.
XX 13-JAN-1998: 98MO-US00153.
XX 14-JAN-1997: 97US-0035496.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;
XX WPI; 1998-399142/34.
XX DR N-PSDB; AAV39085.
XX PT Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
XX the diagnosis of immune system-related disorder(s)
XX Claim 20; Fig 1; 91pp; English.
XX
XX The present sequence represents the human tumour necrosis factor
XX receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides
XX for the TNFR-6 beta protein (AAW63623). TNFR-6 alpha and TNFR-6 beta
XX are members of the tumour necrosis factor receptor (TNFR) family. TNFRs
XX are expressed in endothelial cells, keratinocytes, normal prostate and
XX prostate tumour tissue. For a number of disorders of these cells,
XX particularly of the immune system, substantially altered (whether
XX increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
XX expression can be detected. Therefore the TNFR-6 alpha and TNFR-6 beta
XX polypeptides, nucleic acids and antibodies are claimed to be useful in
XX the diagnosis of such disorders. Mutations of the TNFR-6 alpha and
XX TNFR-6 beta genes can also be detected. The TNFR polypeptides are
XX also claimed to be useful for identifying ligands which may be useful
XX in the treatment of apoptosis related disorders.
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seq\_documentation\_block:

ID AAW97749 standard; Protein: 300 AA.

XX AAW97749;

XX 21-MAY-1999 (first entry)

XX Human tumour necrosis factor receptor ZTNFR-5.

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KW ZTNFR-5; tumour necrosis factor receptor; TNFR; human;
KW cell maturation; bone cell regulation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /note="signal peptide"
FT Protein 24..300
FT /note="mature protein"
FT Domain 24..194
FT /note="extracellular domain"
FT Region 49..71
FT /note="cysteine-rich pseudo-repeat 1"
FT Region 72..113
FT /note="cysteine-rich pseudo-repeat 1"
FT Region 114..151
FT /note="cysteine-rich pseudo-repeat 1"
FT Region 152..194
FT /note="cysteine-rich pseudo-repeat 1"
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PN WO9904001-A1.
XX
PD 28-JAN-1999.
XX
PF 21-JUL-1998; 98MO-US15072.
XX
PR 21-JUL-1997; 97US-0053203.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Farrah TM.
XX
DR WPI: 1999-132245/11.
DR N-PSDB; AAX07226.
XX
PT Novel tumour necrosis factor receptor ZTNFR5 - useful for
PT regulating maturation of TNF-ligand bearing cells
XX
PS Claim 1; Page 84-85; 109pp; English.
XX
CC This polypeptide comprises a new, secreted tumour necrosis factor
CC receptor (see AAW97749), designated ZTNFR-5. Novel ZTNFR-5 encoding
CC polynucleotides and polypeptides were initially identified by
CC querying an expressed sequence tag (EST) database for sequences
CC homologous to conserved motifs within the TNF receptor family.
CC Based on this search, a contig of 16 ESTs (see AAX07226) was
CC constructed. ZTNFR-5 polypeptides comprise 4 cysteine-rich repeats
CC (see also AAW97750-55) that are homologous to other TNF receptors. In
CC particular the soluble, secreted TNF receptor osteoprotegerin.
CC ZTNFR-5 polypeptide can be prepared by recombinant methods. The
CC polypeptide, especially the extracellular domain, can be used to
CC generate a soluble variant of ZTNFR-5. The polypeptides and
CC nucleic acids can be used to screen for ligands, agonists and
CC antagonists of ZTNFR-5. The polypeptides can be used in bone cell
CC regulation and to regulate the maturation of TNF ligand-bearing
CC cells such as T- or B-cells, lymphocytes, peripheral blood
CC mononuclear cells, polymorphonuclear leukocytes, fibroblasts or
CC hematopoietic cells.
XX
SQ Sequence 300 AA;

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alignment\_scores:

Quality: 1634.00 Length: 300  
Ratio: 5.447 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-006-352-1 x AAW97749 ..

Align seg 1/1 to: AAW97749 from: 1 to: 300

[illegible]

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seq_documentation_block:
ID      AAW95082 standard; Protein; 300 AA.
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AC AAW95082;

DT 20-MAY-1999 (first entry)

Orphan receptor (HUMAN NTR-1) polypeptide.

KW HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;  
KW tumour necrosis factor receptor; muscle disorder; bone mass; osteoporosis

KW muscle metabolism; binding agent; cognate ligand.

OS Homo sapiens.

PN WO9907738-A2.  
XX

PD 18-FEB-1999.  
YY

PF 04-AUG-1998; 98WO-US16202.  
XY

PR 06-AUG-1997; 97US-0054869.  
YY

PA (PROC) PROCTER & GAMBLE CO.  
PA (REG-) REGENERON PHARM INC

XX	
PT	Masjajkowski
	Morris J
	Valenzuela
	DM.

XX WPT: 1999-167365/1A  
DB

DR N-PSDB; AAX22300.  
XX

PT Novel orphan human receptor polypeptide and nucleic acid - useful as diagnostic reagents and for treatment of muscle disorders

XX Claim 7: Page 31: 23no: Englisch  
DS

XX  
CC  
this represents a UTMAN NMB-1 20] ucont:400 a novel carbon resistor mbe

CC protein is related to osteoprotegerin (OPG) and to tumour necrosis factor receptor (TNFR). Host cells transformed with a vector comprising the

CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the

CC protein are useful for diagnosis and treatment of humans and animals, especially in muscle disorders as the receptor is involved in regulation of

CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful for screening for novel binding agents and agents which may be

CC used to treat disorders associated with HUMAN NTR-1 imbalance.  
XY

sq	Sequence	300 AA
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alignment\_scores:

Ratio:	5.447
Gaps:	0

1. Introduction

US-09-006-352-1 x AAW95082

Align seg 1/1 to: AAW95082 from: 1 to: 300

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17 abeuProIalaleuProvalProIalavalargIyValalagluthrp 34

125 CCACCTACCCCTGGCGGACGACAGACAGCGGAGCGGCTGGTGTGCGCC 174

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575 CAGGCTCTTCTCCCATGACACCTGTGTGACACGAGTGCACCTGGCTTCCC 624
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    |||||||
201 LeuSerThrArgValProGlyAlaGlnGlnCysGlnArgAlaValIleAs 217
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875 GGATGCGCGGCGTGGAGCGGAGCGTCCGTGAGCGCTTCTCTCTGTGAC 924
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XX
AC AAB19335;
XX
XX
XX 19-FEB-2001 (first entry)
DE A full length human FAS Ligand Inhibitory Protein (FLINT).
XX Human: FAS Ligand Inhibitory Protein: FLINT; analogue; apoptosis;
XX tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;
KW

```

```

KW acute respiratory distress syndrome; ulcerative colitis;
XX chronic obstructive pulmonary disease; Crohn's disease.
XX
OS Homo sapiens.
XX
PN MO200058465-A2.
XX
PD 05-OCT-2000.
XX
PF 20-MAR-2000; 2000WO-US06417.
XX
PR 30-MAR-1999; 99US-0126839.
PR 21-JUN-1999; 99US-0140077.
PR 21-JUN-1999; 99US-0140156.
PR 20-OCT-1999; 99US-0160566.
PR 18-FEB-2000; 2000US-0183398.
XX
PA (TILL) LILLY & CO ELI.
XX
PI Becker GW, Cohen FU, Gonzalez-dewhitt PA, Hale JE, Micanovic R;
PI Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;
PI Wroblewski VJ.
XX
DR WPI: 2000-656167/63.
XX
XX FAS Ligand Inhibitory Protein analogs useful for treating abnormal
PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's
PT disease
XX
XX Disclosure: Page 113-114; 114pp; English.
XX
XX
XX The present sequence represents a full length human FAS Ligand Inhibitory
CC Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
CC FLINT protein is modified to produce analogues, which have greater
CC potency, longer in vivo half-lives, decreased aggregation, decreased
CC absorption onto surfaces, increased solubility and improved ease of
CC formulation. The FLINT analogue is useful for treating a patient
CC suffering from disease or condition relating to abnormal apoptosis such
CC as acute lung injury, acute respiratory distress syndrome, pulmonary
CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
CC Crohn's disease.
XX
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SQ Sequence 300 AA;
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XX Quality: 1634.00 Length: 300
XX Ratio: 5.447 Gaps: 0
XX Percent Similarity: 100.000 Percent Identity: 100.000
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XX 34 roThrTyProTrpArgAspAlaGlnThrGlyGlnArgLeuValCysAla 50
XX |||||||
XX 175 CAGTGGCCCCAGGACCTTTGTGACGGCGCGTGGCCGAGACAGCCC 224
XX |||||||
XX 51 GlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerPr 67

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bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;  
Grave's disease; idiopathic myxedema; autoimmune diabetes;  
thrombotic thrombocytopenic purpura; multiple sclerosis;  
liver diseases; autoimmune gastritis; ulcerative colitis;  
glomerulonephritis; pulmonary fibrosis; heart failure;  
atherosclerosis; aplastic anaemia; myelodysplastic syndromes;  
osteoporosis; Alzheimers disease; Parkinsons disease; stroke;  
myocardial infarction; human.

Homo sapiens.  
MO200046247-A1.  
10-AUG-2000.  
04-FEB-2000; 2000WC-USO3037.  
05-FEB-1999; 99US-0118902.  
20-DEC-1999; 99US-0172754.  
(MERI ) MERCK & CO INC.  
Bal C;  
WPI: 2000-506066/45.  
N-PSDB; AAA53800, AAA53801, AAA53802.

Isolated human M68 nucleic acids and proteins which are part of the  
tumor necrosis factor receptor (TNFR) family, useful for identifying  
modulators that may be used to treat various diseases e.g. cancer,  
osteoporosis, Alzheimer's disease

Claim 1; Page 75-76; 80pp; English.

The M68 protein is a member of a family of proteins which have  
roles in immune responses, cell death, cell proliferation and  
stimulation of cell differentiation. M68 lacks a transmembrane domain  
and is a secreted factor suggesting that it functions as a natural  
inhibitor for its ligand. The altered expression pattern of M68 in a  
multitude of tissues suggests that M68 may play a role in cancer by  
binding to its ligand and blocking apoptotic cell death induced by  
such a ligand. This anti-apoptotic role of M68 suggests that  
modulators of M68 will be useful in treatment of apoptosis-related  
diseases such as various forms of cancer and various bone disorders.  
M68 nucleic acids and proteins are therefore useful for treating  
conditions involving atypical apoptosis and for identifying  
modulators of M68. Modulators of M68 are useful for treatment of  
cancer and other diseases associated with abnormal levels of  
apoptosis including systemic lupus erythematosus, Hashimoto's  
thyroiditis, Grave's disease, idiopathic myxedema, autoimmune  
diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,  
liver diseases, autoimmune gastritis, ulcerative colitis,  
glomerulonephritis, pulmonary fibrosis, heart failure,  
atherosclerosis, aplastic anaemia, myelodysplastic syndromes,  
osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and  
myocardial infarction.

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34  roHnTyPProTPArGaSPAlaGluThrGlyGluIaArgLeuValLysAla 50
175 CAGTGGCCCCCAGGACACCTTTGTGGAGCGGCGGTGCGCGCGAGACGCC 224
51  GlncysProProGlyThrPheValGlnIaArgProCysArgArgAspSerTr 67
225 CAGAGCTGTGGCGCGGTGTCCACCGCGCCACTACACGACGTTCTGGACT 274
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325 GAGGACAGGGGCTTCCACAGCCACCCACCAACCGTGGCTGGCGGTGCCG 374
101 GluAlaIaArgAlaCysHisAlaIaThrHisAsnArgAlaCysArgCysArg 117
375 CGGCTTTTGGCGGACGCTGTTTCTGCTTGGAGACAGCATGTGTGCCAC 424
117  rGlyPhePhePheAlaHisAlaGlyPheCysLeuGlnHisAlaSerCysProp 134
425 CTGTGTGCGCGGTATGGATGGCCCGGCGCACCCCGACGAGCAGAACGGCGT 474
134  roGlyAlaGlyValIleAlaIaProGlyThrProSerGlnAsnThrGlnCys 150
475 CAGCGGTGCCCCCAGGACACTTCTACGCGACAGCTCCAGCTCAGAGCA 524
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525 GTGGCAGCCCCACCGCAACTGCAGCGGCGCTGGCGCTGGCCCTCAATGTGC 574
167  ncysGlnProHisIaArgAsnCysTThAlaLeuGlnLeuAlaLeuAsnValP 184
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184  roGlySerSerSerHisAspThrLeuCysTThSerCysThrGlyPhePro 200
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201  LeuSerThrArgValIaProGlyAlaGluGluCysGluArgAlaValIleAs 217
675 CTTTGTGGCTTTCAGGACATCTCCATCATGAAGAGCGTGCAGCGCGCTGC 724
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

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Searched: 1344157 segs, 7733874588 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: em\_htgo\_rod:\*  
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29: em\_htg\_hum8:\*  
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31: em\_htg\_inv2:\*  
32: em\_htg\_other:\*  
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85: gb\_pr1:\*  
86: gb\_pr2:\*  
87: gb\_pr3:\*  
88: gb\_pr4:\*  
89: gb\_pr5:\*  
90: gb\_pr6:\*  
91: gb\_pr7:\*  
92: gb\_pr8:\*  
93: gb\_pr9:\*  
94: gb\_ro1:\*  
95: gb\_ro2:\*  
96: gb\_in4:\*  
97: gb\_pr10:\*  
98: em\_ba3:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1059	98.3	1168	9	AX017828	AX017828 Sequence
3	1032.8	95.9	4228	85	AB029011	AB029011 Homo sapi
4	1019	94.6	1048	89	AF217794	AF217794 Homo sapi
5	1019	94.6	1114	9	AX055373	AX055373 Sequence
6	1019	94.6	1114	9	AX056645	AX056645 Sequence
7	1019	94.6	1114	88	AF104419	AF104419 Homo sapi
8	1013	94.1	1055	10	AX082868	AX082868 Sequence



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RESULT 2
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LOCUS Definition Sequence 1 from Patent WO946376.
ACCESSION AX017828
VERSION AX017828.1 GI:10042431
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1168)
AUTHORS Kroeger,B.
TITLE Receptor from the superfamily of Int-receptors from the human lung
JOURNAL Patent: WO 946376-A 16-SEP-1999;
BASIS AG (DE); KROEGER BUNKHARD (DE)
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Best Local Similarity 100.0%; Pred. No. 4.4e-188;
Matches 1059; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1021 ctatatttataaagcttttcaataaataaataaataa 1059
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RESULT 3
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LOCUS Homo sapiens mRNA for KIAA1088 protein, partial cds.
DEFINITION AB029011
ACCESSION AB029011
VERSION AB029011.1 GI:5689512
KEYWORDS
SOURCE Homo sapiens brain cDNA to mRNA, clone lib:PIUEScriptII SK plus
clone:hK02589.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (sites) Nagase,T., Ishikawa,K., Hiroseawa,M., Miyajima,N.,
Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes.
XIV. The complete sequences of 100 new cDNA clones from brain which
code for large proteins in vitro
JOURNAL DNA Res. 6 (3), 197-205 (1999)
MEDLINE 99397452
REFERENCE 2 (bases 1 to 4228)
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DEFINITION	Sequence 1 from Patent WO0075316.		
ACCESSION	AX056645		
VERSION	AX056645.1	GI:12309639	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1114)		
JOURNAL	Ashkenazi, A.J., Goddard, A., Gurney, A.L., Hillan, K., Napier, M., Wood, W.I.		
	Methods and compositions for inhibiting neoplastic cell growth.		
	Patent: WO 0075316-A 1 14-DEC-2000;		
	Genotech, Inc. (us)		

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VERSION	AF104419.1	GI:4106877	
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Pitli,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C., Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T., Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L., Goddard,A.D., Bolstein,D. and Ashkenazi,A.		
TITLE	Genomic amplification of a decoy receptor for Fas ligand in lung and colon cancer		
JOURNAL	Nature 396 (5712), 699-703 (1998)		
MEDLINE	99087326		
REFERENCE	2 (bases 1 to 1114)		
AUTHORS	Pitli,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C., Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T., Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L., Goddard,A.D., Bolstein,D. and Ashkenazi,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-NOV-1998) Molecular Oncology, Genentech, 1 DNA Way, San Francisco, CA 94080, USA		
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DEFINITION	Sequence 1 from Patent WO0110908.				
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Db	137	TGCGGTGGTGGTGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG	196		
QY	121	AACCCACCTACCCCTTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	180		
Db	137	ACACCCACTTACCCCTTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	256		
QY	181	CCCCGACGACCTTGTGTGCGAGCGCTGTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	240		
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QY	241	TGTCCACCGCGCGACCTAAGCGAGTTCGTGAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAG	300		
Db	317	TGTCCACCGCGCGCGACCTAAGCGAGTTCGTGAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAG	376		
QY	301	GTCCTGTGCGGAG	360		
Db	377	GTCCTGTGCGGAG	436		
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Db	437	TGCGCTGTGCGCGAGCGCTGTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	496		
QY	421	CCACCTGTGTGCGCGCTGTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	480		
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QY	481	TGCGCGCGAG	540		
Db	557	TGCGCGCGAG	616		
QY	541	AACCTGACGCGCGCTGTGCGCGAG	600		
Db	617	AACCTGACGCGCGCGCTGTGCGCGAG	676		
QY	601	TGCGCGCGAG	660		
Db	677	TGCGCGCGAG	736		
QY	661	CGTGCCTGATCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	720		
Db	737	CGTGCCTGATCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG	796		
QY	721	CTGCGAGCGCGCGAG	780		
Db	797	CTGCGAGCGCGCGAG	856		
QY	781	CTGCGAGCGAG	840		
Db	857	CTGCGAGCGAG	916		
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QY	901	CGTGTGCGCTGTGCGAGCGCTGTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	960		
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QY	961	GCACCCGAG	1019		
Db	1037	GCACCCGAG	1095		

KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1055)  
AUTHORS Hsu, H.  
TITLE NF- $\kappa$ B, a member of the TNF-receptor supergene family  
JOURNAL Patent: WO 0110908-A 1 15-FEB-2001;  
Amgen Inc. (US)

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DEFINITION Homo sapiens M68C mRNA, alternatively spliced, complete cds.  
ACCESSION AF217793  
VERSION AF217793.1 GI:5969260  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 1428)  
AUTHORS Bai, C., Connolly, B., Metzger, M. L., Hilliard, C. A., Liu, X., Sandley, Y., Soderman, A., Galloway, S. M., Liu, Q., Austin, C. P., and Caskey, C. T.  
TITLE Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)  
MEDLINE 20122600  
PUBMED 10655513  
REFERENCE 2 (bases 1 to 1428)  
AUTHORS Bai, C.  
TITLE Direct Submission  
JOURNAL Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories, Summeytown Pike, West Point, PA 19403, USA  
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KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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AUTHORS 1 (bases 1 to 936)  
TITLE Altkinson, P. R., Tian, Y., and Mitcher, D. R.  
JOURNAL Flint analog compounds and formulations thereof  
Patent: WO 0118202-A 3 15-MAR-2001;  
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BASE COUNT 132 a 341 c 311 g 152 t  
ORIGIN

Query Match 86.6%; Score 932.8; DB 10; Length 936;  
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QY 181 ccccaagac 240  
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RESULT 13  
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LOCUS AF134240 903 bp mRNA PRI 11-MAY-1999  
DEFINITION Homo sapiens tumor necrosis factor receptor homolog (TR6) mRNA,  
complete cds.  
ACCESSION AF134240  
VERSION AF134240.1 GI:4768938  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS Yu, K.Y., Kwon, B., Ni, J., Zhai, Y., Ebner, R., and Kwon, B.S.  
TITLE A newly identified member of tumor necrosis factor receptor  
superfamily (TR6) suppresses LIGM-mediated apoptosis  
J. Biol. Chem. 274 (20), 13733-13736 (1999)  
MEDLINE 99253915  
REFERENCE 2 (bases 1 to 903)  
AUTHORS Kwon, B.S. and Yu, K.Y.  
TITLE Direct Submission  
JOURNAL Submitted (10-MAR-1999) Micro/Immunol, Indiana University, 635  
Barnhill Drive, Indianapolis, IN 46202, USA  
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BASE COUNT 129 a 324 c 305 g 145 t  
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 QY 645 ag 646  
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 Db 86596 TG 86597

Search completed: October 31, 2001, 10:31:32  
 Job time: 3018 sec

Mon Nov 5 08:22:32 2001

us-09-006-352-1.rge

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Page 16

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 31, 2001, 09:41:15 ; Search time 290.92 Seconds  
(without alignments)  
2324.522 Million cell updates/sec

Title: US-09-006-352-1  
Perfect score: 1077  
Sequence: 1 gcttcctgctccagcaag.....aaaaaaaaaaaaaaaa 1077

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 730101 seqs, 313950809 residues  
Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_0601.\*  
1: /SIDSI/gcgdata/geneseq/geneseqn/NA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseqn/NA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseqn/NA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseqn/NA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseqn/NA1984.DAT.\*  
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11: /SIDSI/gcgdata/geneseq/geneseqn/NA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseqn/NA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseqn/NA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseqn/NA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseqn/NA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseqn/NA1995.DAT.\*  
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18: /SIDSI/gcgdata/geneseq/geneseqn/NA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseqn/NA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseqn/NA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseqn/NA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseqn/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1077	100.0	1077	19	AAV39085 Human tumour necro
2	1077	100.0	1077	21	AAA03772 Human tumour necro
3	1077	100.0	1164	19	AAV07654 Nucleotide sequenc
4	1059.8	98.4	1137	21	AA292404 CDNA encoding huma
5	1059	98.3	1168	20	AA209998 Human lung TNF-rec
6	1030	95.6	1347	21	AA63764 Human soluble TNF
7	1028.8	95.5	1462	20	AA76052 Mammalian tumour r
8	1019	94.6	1066	21	AA53802 M68 TNF receptor r
9	1019	94.6	1114	21	AA58367 Human PRO212 nucle
10	1019	94.6	1114	21	AA58581 Human PRO212 prote
11	1019	94.6	1114	21	AA77537 Human PRO212 CDNA

12	1019	94.6	1114	22	AA084421 Human PRO212 polyp
13	1019	94.6	1114	22	AA091462 Human PRO212 CDNA.
14	1019	94.6	1205	20	AA07226 Human tumour necro
15	1018	94.5	1114	20	AA32744 Human DCR3 polypep
16	1013	94.1	1055	22	AA62705 Human NTR3 nucleot
17	1002.8	93.1	1428	21	AA53801 M68 TNF receptor r
18	934.4	86.8	936	20	AA25376 Human FLINT #2 nuc
19	932.8	86.6	936	21	AA88731 Human FAS ligand 1
20	932.8	86.6	936	21	AA51076 Human FLINT coding
21	932.8	86.6	936	22	AA77696 Human FLINT native
22	903	83.8	900	20	AA22300 Orphan receptor (H
23	900	83.6	900	20	AA225375 Human FLINT #1 nuc
24	900	83.6	900	21	AA53208 Human Fas ligand 1
25	900	83.6	900	21	AA51075 Human FLINT coding
26	823.4	76.5	825	20	AA25378 Human mFLINT #2 nu
27	823.4	76.5	825	21	AA51078 Human mature FLINT
28	813	75.5	813	20	AA25377 Human mFLINT #1 nu
29	813	75.5	813	21	AA75899 DNA encoding a mat
30	813	75.5	813	21	AA88730 Human FAS ligand 1
31	813	75.5	813	21	AA51077 Mature human FLINT
32	797.6	74.1	900	21	AA53209 Monkey Fas ligand
33	755.2	70.1	899	20	AA89503 DNA encoding a hum
34	742	68.9	767	20	AA23419 Human APO6 DNA. H
35	644.4	59.8	1859	21	AA63765 Human soluble TNF
36	498.4	46.3	1667	19	AAV39086 Human tumour necro
37	498.4	46.3	1667	21	AA37773 Human tumour necro
38	492	45.7	7720	21	AA53800 Genomic DNA encodi
39	473.4	44.0	491	20	AA32745 Human DCR3 EST seq
40	459	42.6	459	20	AA84621 Human TNFR superfa
41	459	42.6	459	21	AA63757 Human TNFR soluble
42	394.4	36.6	397	20	AA07227 Human tumour necro
43	305.2	28.3	497	19	AA39094 HEID106R DNA seque
44	305.2	28.3	497	21	AA37774 Human tumour necro
45	245.2	22.8	271	20	AA32747 Human DCR3 EST seq

# ALIGNMENTS

RESULT 1					
ID	AAV39085	standard; cDNA; 1077 BP.			
XX	AAV39085;				
AC					
XX					
DT	26-OCT-1998	(first entry)			
XX					
DE	Human tumour necrosis factor receptor-6 alpha cDNA.				
XX					
KW	Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;				
KW	endothelial cells; keratinocytes; normal prostate; apoptosis;				
KW	prostate tumour tissue; ss.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	CDS	25..927			
FT		/*tag= a			
FT	sig_peptide	25..114			
FT		/*tag= b			
FT	mat_peptide	115..924			
FT		/*tag= c			
XX					
PN	W09830694-A2.				
XX					
PD	16-JUL-1998.				
XX					
PF	13-JAN-1998;	98WO-US00153.			
XX					
PR	14-JAN-1997;	97US-0035496.			
XX					
PA	(HUMA-) HUMAN GENOME SCI INC.				

XX Ebner R, Feng P, Gentz RL, Nl J, Ruben SM, Yu G:  
 PI WPI: 1998-399142/34.  
 DR P-PSDB; AAM63622.  
 XX  
 PT Human tumour necrosis factor receptors 6-alpha and 6-beta - used in  
 PT the diagnosis of immune system-related disorder(s)  
 PS Disclosure; Fig 1: 91p; English.

XX The present sequence represents the human tumour necrosis factor  
 CC receptor-6 alpha (TNFR-6 alpha) cDNA. The invention also provides  
 CC for the TNFR-6 beta cDNA (AAV39086). TNFR-6 alpha and TNFR-6 beta are  
 CC members of the tumour necrosis factor receptor (TNFR) family. TNFRs  
 CC are expressed in endothelial cells, keratinocytes, normal prostate and  
 CC prostate tumour tissue. For a number of disorders of these cells,  
 CC particularly of the immune system, substantially altered (whether  
 CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene  
 CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta  
 CC polypeptides, nucleic acids and antibodies are claimed to be useful in  
 CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and  
 CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are  
 CC also claimed to be useful for identifying ligands which may be useful  
 CC in the treatment of apoptosis related disorders.

XX Sequence 1077 BP: 196 A; 360 C; 326 G; 195 T; 0 other:

Query Match 100.0%; Score 1077; DB 19; Length 1077;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-190;

Matches 1077: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 tgcctggtgttgcgcgtgcgcgtcctcgtccggtccgcgtcgtacgcgagtgacaa 120  
 Db 61 tgcctggtgttgcgcgtgcgcgtcctcgtccggtccgcgtcgtacgcgagtgacaa 120  
 QY 121 aacaccacctaccctctgcgagcagcagagagagagagagagagagagagagag 180  
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 Db 241 tctccacgcgcgcacactacacagcagcttctgaaactcctctgagagcgtctactgaac 300  
 QY 301 gtctctctgcggagcgttgaaggagagagagagagagagagagagagagagagagag 360  
 Db 301 gtctctctgcggagcgttgaaggagagagagagagagagagagagagagagagagag 360  
 QY 361 tgcgcgtgcgcagcagcgtctctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 420  
 Db 361 tgcgcgtgcgcagcagcgtctctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 420  
 QY 421 ccaactgtgcgcgcgtgatgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 480  
 Db 421 ccaactgtgcgcgcgtgatgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 480  
 QY 481 tgcgcgcgcgcagcaccctctcagcagcagcagcagcagcagcagcagcagcagcagc 540  
 Db 481 tgcgcgcgcgcagcaccctctcagcagcagcagcagcagcagcagcagcagcagcagc 540  
 QY 541 aactgcagcgcgcgtgc 600  
 Db 541 aactgcagcgcgcgtgc 600

QY 601 tgcaccagctgactgctgctcccccctcagcaccagggtaaccagagctgagagtgtag 660  
 Db 601 tgcaccagctgactgctgctcccccctcagcaccagggtaaccagagctgagagtgtag 660  
 QY 661 cgtgcgcctacactcttgcgtcttccagacatcctcacaagaagctgcagcgcgtg 720  
 Db 661 cgtgcgcctacactcttgcgtcttccagacatcctcacaagaagctgcagcgcgtg 720  
 QY 721 ctgcagcgcctcagagcccccagagagctggtggtccgcagacccaagggcgcgcgcgc 780  
 Db 721 ctgcagcgcctcagagcccccagagagctggtggtccgcagacccaagggcgcgcgcgc 780  
 QY 781 ttgcagctgaagctgc 840  
 Db 781 ttgcagctgaagctgc 840  
 QY 841 ctgtgcgcgtctgcagcgcgtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 900  
 Db 841 ctgtgcgcgtctgcagcgcgtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 900  
 QY 901 cgtgagcgtcttccctcctctgcactgactcctgcgcgcgcgcgcgcgcgcgcgcgc 960  
 Db 901 cgtgagcgtcttccctcctctgcactgactcctgcgcgcgcgcgcgcgcgcgcgcgc 960  
 QY 961 gcacccacttgactgaaagagcgttcttcttaaatagaagaatgaggttcttaag 1020  
 Db 961 gcacccacttgactgaaagagcgttcttcttaaatagaagaatgaggttcttaag 1020  
 QY 1021 ctatcttataaagcttcttcatataaataaataaataaataaataaataaataa 1077  
 Db 1021 ctatcttataaagcttcttcatataaataaataaataaataaataaataaataa 1077

RESULT 2  
 AAA37772  
 ID AAA37772 standard: DNA; 1077 BP.  
 XX  
 AC AAA37772;  
 DT 04-DEC-2000 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor-6 alpha coding sequence.  
 XX  
 KW Human: Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;  
 KW breast neovascularisation; solid tumour; malignancy; prostate cancer;  
 KW pre-maturity macular degeneration; allergy; inflammation; tissue damage;  
 KW thyroid associated ophthalmopathy; cell damage; parasitic infection;  
 KW bone disease; osteoporosis; atherosclerosis; cardiovascular disease;  
 KW neurodegenerative disorder; Alzheimer's disease; immune disorder;  
 KW graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;  
 KW psoriasis; septic shock; ulcerative colitis; therapy; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 25..927  
 FT /tag= a  
 FT /product= TNFR-6alpha  
 XX  
 PN WO200052028-A1.  
 XX  
 PD 08-SEP-2000.  
 XX  
 PF 03-MAR-2000; 2000WO-US05686.  
 XX  
 PR 04-MAR-1999; 99US-0121774.  
 PR 12-MAR-1999; 99US-0124092.  
 PR 27-APR-1999; 99US-0131279.  
 PR 30-APR-1999; 99US-0131964.  
 PR 02-AUG-1999; 99US-0146371.  
 PR 01-DEC-1999; 99US-0168235.  
 XX

PA (HUMA-) HUMAN GENOME SCI INC.  
 XX Gentz RL, Ni J, Ebner R, Yu G, Ruben SM, Feng P;  
 XX MPI: 2000-572174/53.  
 DR P-PSDB: AAY90357.  
 XX  
 PT Nucleic acids encoding human tumour necrosis factor receptor (TNFR)  
 PT Proteins TNFR-galpa and TNFR-6beta, useful for treating e.g.  
 PT Alzheimer's disease, osteoporosis and graft rejection  
 XX  
 PS Claim 2; Fig 1; 332pp; English.  
 XX  
 CC This sequence encodes the human tumour necrosis factor receptor 6  
 CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA  
 CC and protein sequences can be used in the prevention, treatment and  
 CC diagnosis of diseases associated with inappropriate TNFR expression. The  
 CC nucleic acids, polypeptides, antibodies, agonists and antagonists against  
 CC them may be used for the treatment of a range of conditions such as  
 CC disorders associated with neovascularisation (especially ocular  
 CC neovascularisation) (such as solid tumours and malignancies (e.g.  
 CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy  
 CC and pre-maturity macular degeneration), allergies, inflammation,  
 CC thyroid associated ophthalmopathy tissue/cell damage, wounds, microbial  
 CC and parasitic infections, bone disease (e.g. osteoporosis),  
 CC atherosclerosis, pain, cardiovascular disease (e.g. stroke), immune  
 CC neurodegenerative disorders (e.g. Alzheimer's disease), immune  
 CC disorders (e.g. graft rejection), rheumatism, liver disease,  
 CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative  
 CC colitis.  
 XX  
 SQ Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;  
 XX  
 Query Match 100.0%; Score 1077; DB 21; Length 1077;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-190;  
 Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 541 aactgcacggcccttgccctgagccctcaatgtgcacagctcttccctccatgacacctg 600  
 QY 601 tgcacacgctgcacacttgcttccctccatgacacacagaggtaccagagcttgagagtgag 660  
 DB 601 tgcacacgctgcacacttgcttccctccatgacacacagaggtaccagagcttgagagtgag 660  
 QY 661 cgtgcctcatcgacttgcttgccttcacagacatcccatcaagagctgcacagctg 720  
 DB 661 cgtgcctcatcgacttgcttgccttcacagacatcccatcaagagctgcacagctg 720  
 QY 721 ctgcagccctcgcagagcccgagaggtggtgtccgacacacagagcgagcgagcgcc 780  
 DB 721 ctgcagccctcgcagagcccgagaggtggtgtccgacacacagagcgagcgagcgcc 780  
 QY 781 ttgcagctgaagctgcgttcgagcgtacagagctccttgaggcgacagagcgctg 840  
 DB 781 ttgcagctgaagctgcgttcgagcgtacagagctccttgaggcgacagagcgctg 840  
 QY 841 ctggtgcgctgcgtgcagcgctgcgtgcgtgcagagtgcccgagctgagcgagcgctc 900  
 DB 841 ctggtgcgctgcgtgcagcgctgcgtgcgtgcagagtgcccgagctgagcgagcgctc 900  
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 DB 901 cgtgagcgtctcctcccttgacactgaatccctgagccctcttatttaccatcccttg 960  
 QY 961 gcacccacattgcactgaagaagcttttttaataagaagaatgaggtttcctaag 1020  
 DB 961 gcacccacattgcactgaagaagcttttttaataagaagaatgaggtttcctaag 1020  
 QY 1021 cttaatttttaagcttttctataaataaataaataaataaataaataaataa 1077  
 DB 1021 cttaatttttaagcttttctataaataaataaataaataaataaataaataa 1077

RESULT 3  
 AAV07654  
 ID AAV07654 standard; cDNA; 1164 BP.  
 XX  
 AC AAV07654;  
 XX  
 DT 02-DEC-1998 (first entry)  
 XX  
 DE 'Nucleotide sequence of tumour necrosis related receptor (TR4).  
 KW Human; tumour necrosis related receptor; TR4; agonist; antagonist;  
 KW inhibition; chronic; acute; inflammation; arthritis; septicemia;  
 KW autoimmune disease; transplant rejection; stroke; cancer;  
 KW Alzheimer's disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 111..1013  
 FT /tag= a  
 FT /product= "human TR4"  
 XX  
 PN EP861850-A1.  
 XX  
 PD 02-SEP-1998.  
 XX  
 PF 20-JAN-1998; 98EP-0300382.  
 XX  
 PR 04-FEB-1997; 97US-0794796.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Emery J, Tan KB, Truneh A, Young PR;  
 XX  
 DR MPI: 1998-508248/44.

DR P-PSDB; AAM66102.  
 XX New DNA encoding tumour necrosis related receptor - used to treat  
 PT and prevent e.g. inflammation, arthritis, septicaemia, autoimmune  
 PT diseases, transplant rejection, infection, stroke, ischaemia, ARDS,  
 PT restenosis, AIDS, bone disorders and cancer  
 XX  
 XX Claim 3: Fig 1: 21pp: English.  
 XX  
 CC This is the nucleotide sequence of the human tumour necrosis related  
 CC receptor (TR4), used in the method of the invention. The TR4 protein  
 CC or its agonist can be used to treat a subject in need of enhanced  
 CC TR4 polypeptide activity. The antagonist is used to inhibit TR4  
 CC polypeptide activity. The active agents can be used for the  
 CC treatment and prevention of diseases such as chronic and acute  
 CC inflammation, arthritis, septicaemia, autoimmune diseases, transplant  
 CC rejection, stroke, cancer, Alzheimer's disease.  
 XX  
 XX Sequence 1164 BP: 206 A; 396 C; 355 G; 207 T; 0 other:

Query Match 100.0%: Score 1077: DB 19: Length 1164:  
 Best Local Similarity 100.0%: Pred No. 2, 3e-190:  
 Matches 1077: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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 OY 61 tgcctggtgttgctgctgctgctgctgctgctgctgctgctgctgctg 120  
 DB 147 tgcctggtgttgctgctgctgctgctgctgctgctgctgctgctgctg 206  
 OY 121 acacccactacccctgagcagagacagagagagagcctgctgctgctg 180  
 DB 207 acacccactacccctgagcagagacagagagagagcctgctgctgctg 266  
 OY 181 cccccagagacattgtgcaagcagcctgctgctgctgctgctgctgctg 240  
 DB 267 cccccagagacattgtgcaagcagcctgctgctgctgctgctgctgctg 326  
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 DB 327 tgcacacgcgcacactaacacagcttctggaactctgagagcctgctgctg 386  
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 DB 387 gtccctcgcggagagcgtgagagagagagcagcagcctgctgctgctg 446  
 OY 361 tgcctcgcgcagcagccttctgctgcaagcgtgctgctgctgctgctg 420  
 DB 447 tgcctcgcgcagcagccttctgctgcaagcgtgctgctgctgctgctg 506  
 OY 421 ccaactggtgctgagcgttatgtgcccgcagcagccagcagagacagtgccagc 480  
 DB 507 ccaactggtgctgagcgttatgtgcccgcagcagccagcagagacagtgccagc 566  
 OY 481 tgcctcgcgcagcagccttctgcaagcagcagctcagctcagagcaatgcccacgc 540  
 DB 567 tgcctcgcgcagcagccttctgcaagcagcagctcagctcagagcaatgcccacgc 626  
 OY 541 aactgagagccttgagccttgccctcaatgtgcccagcttctctccatgacacctg 600  
 DB 627 aactgagagccttgagccttgccctcaatgtgcccagcttctctccatgacacctg 686  
 OY 601 tgcacagagctgactgagcttccctcagacacagagtgtaacagagctgagagtgag 660  
 DB 687 tgcacagagctgactgagcttccctcagacacagagtgtaacagagctgagagtgag 746  
 OY 661 cgtgcagctacagacttgtagcttccagagacatcctacacagagctgacagagctg 720  
 DB 747 cgtgcagctacagacttgtagcttccagagacatcctacacagagctgacagagctg 806

OY 721 ctgcagagcctcctgagagcccccagagagctgggtctgcagacacaaaggcgcgcgcgc 780  
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 DB 1107 ctatttttataaagcttcttcaataaataaataaataaataaataaataaataaataa 1163

RESULT 4  
 AA92404  
 ID AA92404 standard: cDNA: 1137 BP.

AA92404:  
 05-JUN-2000 (first entry)

CDNA encoding human TNF receptor-like protein, HDTEA84.

TNF receptor family; tumour necrosis factor; HDTEA84; HSLJD37R;  
 Rank-like protein; RANKL; immune disorder; inflammation; allergy;  
 immunosuppressant; antiarthritis; antirheumatoid; antiinflammatory;  
 dermatological; antihypoid; ss.

OS Homo sapiens.

XX Key. Location/Qualifiers  
 FT CDS 99..1001  
 FT /tag= a  
 FT /product= "Human HDTEA84"

PN WO200001817-A2.  
 PD 13-JAN-2000.  
 XX 06-JUL-1999: 99WO-US12366.

XX 06-JUL-1998: 98US-0110938.  
 FR 13-JUL-1998: 98US-0114468.  
 FR 23-JUL-1998: 98US-0093897.  
 FR 12-AUG-1998: 98US-0132968.  
 PR 18-AUG-1998: 98US-0136214.  
 PR 11-SEP-1998: 98US-0099999.

XX (SCHE ) SCHERING CORP.

PI Bates EM, Labèque SE, Murphy BE, Mattson JD, Gorman DM;  
 PI Hedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA;  
 PI Bazan JF, Mahony D, Lees EM;

DR WPI: 2000-171015/15.  
 DR P-PSDB: AAY7458.

XX New isolated mammalian genes, used to develop products for treating  
 PT e.g. immune, inflammatory or allergic abnormalities, cancers or  
 PT degenerative conditions -







PS Claim 8; Page 73-74; 77pp; English.

XX The present sequence is given in a specification relating to an isolated  
CC human protein designated tumour necrosis factor like-1 (TNFL1). It may be  
CC used to induce cell death in tumours, to induce apoptosis of activated T  
CC cells, to induce inflammation, and to rescue resting T cells from  
CC apoptosis. TNF receptors are used to regulate the function of a TNF  
CC ligand which plays a role in apoptosis, inflammation, differentiation, or  
CC proliferation. Expression of the receptors can also be useful as markers  
CC for cancer, especially for colon cancer. Diseases which can be treated  
CC using ligands and/or receptors of the TNF/TNFR superfamily include  
CC rheumatoid arthritis, cancer, septic shock, Crohn's disease and  
CC osteoporosis. The polynucleotides can be used in gene delivery vehicles,  
CC for the purpose of delivering a mRNA or oligonucleotide, full-length  
CC protein, fusion protein, polypeptide, or ribozyme, or single-chain  
CC antibody, into a cell. The newly identified receptor proteins play  
CC regulatory roles in cell proliferation and/or differentiation. The  
CC receptors can also play a role in the negative regulation of  
CC osteoclastogenesis. Soluble TNFR-like receptors can be useful in the  
CC neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be  
CC used to treat autoimmune diseases (myasthenia gravis and  
CC insulin-dependent diabetes mellitus), tumours, and proliferative  
CC disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be  
CC delivered to subjects for the purpose of screening test compounds for  
CC those which are useful for enhancing transfer of TNF-L subgenomic  
CC polynucleotides to the cell or for enhancing subsequent biological  
CC effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.  
XX  
XX Sequence 1347 BP; 230 A; 444 C; 443 G; 230 T; 0 other;

Query Match 95.6%; Score 1030; DB 21; Length 1347;  
Best Local Similarity 98.6%; Pred. No. 1.1e-181;  
Matches 1039; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 gctctccctctcagaaagacatgagcgctgtgagggccagggcctgtcgtctg 60  
DB 294 gctctccctctcagaaagacatgagcgctgtgagggccagggcctgtcgtctg 353  
QY 61 tgcctgtgtgtgagcgctgtcgcctctcgcggtgcgcgctgtacgcgagttgcagaa 120  
DB 354 tgcctgtgtgtgagcgctgtcgcctctcgcggtgcgcgctgtacgcgagttgcagaa 413  
QY 121 acacccacacacccctgtgcgagcagacagagagcgagcgctgtgtgtgtgtgtgtgtc 180  
DB 414 acacccacacacccctgtgcgagcagacagagagcgagcgctgtgtgtgtgtgtgtgtc 473  
QY 181 ccccccagac 240  
DB 474 ccccccagac 533  
QY 241 tgtccacacgac 300  
DB 534 tgtccacacgac 593  
QY 301 gtccctctgcgagagcgctgagagagcagcggtctgtccacgcacacacacacacacacacac 360  
DB 594 gtccctctgcgagagcgctgagagagcagcggtctgtccacgcacacacacacacacacacac 653  
QY 361 tgcgcgtctgcgacacggtctctcgcgcacgctgtgttctgtgtgtgtgtgtgtgtgtgtgt 420  
DB 654 tgcgcgtctgcgacacggtctctcgcgcacgctgtgttctgtgtgtgtgtgtgtgtgtgtgt 713  
QY 421 ccaacctgtgcgagcgatgtgc 480  
DB 714 ccaacctgtgcgagcgatgtgc 773  
QY 481 tgcacccacgac 540  
DB 774 tgcacccacgac 833  
QY 541 aactgtcagcgctgt 600

DB 834 aactgtcagcgctgt 893  
QY 601 tgcacacacgctgcac 660  
DB 894 tgcacacacgctgcac 953  
QY 661 cgtgcgcctacatgcac 720  
DB 954 cgtgcgcctacatgcac 1013  
QY 721 ctggaagccctcagagcgcccggaagcgctgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 780  
DB 1014 ctggaagccctcagagcgcccggaagcgctgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1073  
QY 781 ttgagctgaagctgc 840  
DB 1074 ttgagctgaagctgc 1133  
QY 841 ctggtgcgctgtcgtcgc 900  
DB 1134 ctggtgcgctgtcgtcgc 1193  
QY 901 cgtgagcgcttccctcctgtgcac 960  
DB 1194 cgtgagcgcttccctcctgtgcac 1253  
QY 961 gcacccac 1020  
DB 1254 gcacccac 1313  
QY 1021 ctaatttataaagccttttataaataaataaataaataaataaataaataaataaataaataaataa 1054  
DB 1314 ctaataaataaataaataaataaataaataaataaataaataaataaataaataaataaataaataaataa 1347  
RESULT 7  
AAK76052  
ID AAK76052 standard; DNA: 1462 BP.  
XX  
XX AAK76052:  
AC  
XX  
DT 02-AUG-1999 (first entry)  
XX  
XX Mammalian tumour necrosis factor receptor OPG-2 encoding DNA.  
DE  
XX Tumour necrosis factor receptor; TNF receptor; OPG-2; Paget's disease;  
KW osteopenic disorder; osteoclast activity; primary osteoporosis;  
XX hyperglycaemia; osteolytic metastasis; immune response; cancer; ss.  
XX  
XX Mammalia.  
OS  
XX  
XX WO926977-A1.  
PN  
XX  
XX 03-JUN-1999.  
PD  
XX  
XX 24-NOV-1998; 98MO-US25065.  
PF  
XX  
XX 17-FEB-1998; 98US-0074896.  
PR  
XX 24-NOV-1997; 97US-0066446.  
PR  
XX  
XX (BIOJ ) BIOGEN INC.  
PA  
XX  
XX Tschoep J;  
PI  
XX  
XX WPI: 1999-347693/29.  
DR  
XX P-PDB; AAY17479.  
DR  
XX  
XX New tumour necrosis factor family receptor OPG-2  
XX  
XX  
XX Claim 4; Page 18; 22pp; English.  
XX  
XX The present sequence encodes a mammalian tumour necrosis factor  
XX receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis



CC inhibitor for its ligand. The altered expression pattern of M68 in a  
 CC multitude of tissues suggests that M68 may play a role in cancer by  
 CC binding to its ligand and blocking apoptotic cell death induced by  
 CC a ligand. This anti-apoptotic role of M68 suggests that  
 CC modulators of M68 will be useful in treatment of apoptosis-related  
 CC diseases such as various forms of cancer and various bone disorders.  
 CC M68 nucleic acids and proteins are therefore useful for treating  
 CC conditions involving atypical apoptosis and for identifying  
 CC modulators of M68. Modulators of M68 are useful for treatment of  
 CC cancer and other diseases associated with abnormal levels of  
 CC apoptosis including systemic lupus erythematosus, Hashimoto's  
 CC thyroiditis, Grave's disease, idiopathic myxedema, autoimmune  
 CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,  
 CC liver diseases, autoimmune gastritis, ulcerative colitis,  
 CC glomerulonephritis, pulmonary fibrosis, heart failure,  
 CC atherosclerosis, aplastic anaemia, myelodysplastic syndromes,  
 CC osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and  
 CC myocardial infarction.

QY 721 ctgacagccctcagagagcccccagagagcttggtccgacacacagagccgcgcgc 780  
 Db 749 ctgacagccctcagagagcccccagagagcttggtccgacacacagagccgcgcgc 808  
 QY 781 ttccagctgaagcttgctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 840  
 Db 809 ttgcagctgaagcttgctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 868  
 QY 841 ctggtgagcttgctgc 900  
 Db 869 ctggtgagcttgctgc 928  
 QY 901 cgtgagagcttcctccctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 960  
 Db 929 cgtgagagcttcctccctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 988  
 QY 961 gcaccccaacttgcaatgaagaagcttttttaataagaagaatgagttccttaa 1019  
 Db 989 gcaccccaacttgcaatgaagaagcttttttaataagaagaatgagttccttaa 1047

Query Match 94.6% Score 1019; DB 21; Length 1066;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-179;  
 Matches 1019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9  
 AAC58367  
 ID AAC58367 standard; CDNA; 1114 BP.  
 XX  
 AC AAC58367;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human PRO212 nucleotide sequence SEQ ID NO:1.  
 XX

KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
 KW Proliferation; tumorigenesis; identification; cancer; cytostatic;  
 KW neurotropic; neuroprotective; antiinflammatory; immunosuppressive;  
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
 KW neuronal disorder; gliial disorder; astrocytal disorder; angiogenic;  
 KW hypochalamic disorder; glandular disorder; macrophagal disorder;  
 KW epithelial disorder; stromal disorder; blastocoeilic disorder;  
 KW inflammatory disorder; immunologic disorder; ss.

OS Homo sapiens.  
 XX  
 PN WO200053755-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PE 06-JAN-2000; 2000MO-US00376.  
 XX  
 PR 08-MAR-1999; 99MO-US05028.  
 PR 02-JUN-1999; 99MO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 30-NOV-1999; 99MO-US28313.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 05-JAN-2000; 2000MO-US00219.  
 XX

PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
 PI Watanabe CK, Wood WL;  
 DR WPI: 2000-572270/53.  
 DR P-PSDB; AAB24057.  
 XX  
 XX

PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
 PT treatment, diagnosis and prevention of cancer -  
 PS  
 PS Claim 50; Fig 1; 286pp; English.

CC The present invention describes an isolated antibody that binds to  
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,  
 CC

QY 1 gctctccctcgtccacgaagacatgagagcgctgagagggcagccctgtcgtcgtc 60  
 Db 29 gctctccctcgtccacgaagacatgagagcgctgagagggcagccctgtcgtcgtc 88  
 QY 61 tgcctggtgttgagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 120  
 Db 89 tgcctggtgttgagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 148  
 QY 121 aaccccaactacccctggcgagcgagacagagcgagagcgctgtgtgtgcgccagtgc 180  
 Db 149 aaccccaactacccctggcgagcgagacagagcgagagcgctgtgtgtgcgccagtgc 208  
 QY 181 cccccaagcactcttgacagcgagcgctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 240  
 Db 209 cccccaagcactcttgacagcgagcgctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 268  
 QY 241 tgtcaacgcgcgcactacacagcagttctggaactacctgagcgctgcgtactgtcaac 300  
 Db 269 tgtcaacgcgcgcactacacagcagttctggaactacctgagcgctgcgtactgtcaac 328  
 QY 301 gtcctctggcgagagcgctgagagagagcgagcgctgtgcacgcacacacacgtgcc 360  
 Db 329 gtcctctggcgagagcgctgagagagagcgagcgctgtgcacgcacacacacgtgcc 388  
 QY 361 tgcgcctgcgcgcacgcgcctctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 420  
 Db 389 tgcgcctgcgcgcacgcgcctctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 448  
 QY 421 ccaactgtgctgcgcgttgatgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 480  
 Db 449 ccaactgtgctgcgcgttgatgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 508  
 QY 481 tgcgcgcgcgcgcgcctctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 540  
 Db 509 tgcgcgcgcgcgcgcctctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 568  
 QY 541 aactgcagagcccttgagcgcctcgaatgtgccaagcgcttcctccccaatgacacctg 600  
 Db 569 aactgcagagcccttgagcgcctcgaatgtgccaagcgcttcctccccaatgacacctg 628  
 QY 601 tgcacacagctgaactgtgcttcctccccaatgacacagaggtacacagagctgagagtg 660  
 Db 629 tgcacacagctgaactgtgcttcctccccaatgacacagaggtacacagagctgagagtg 688  
 QY 661 cgtgcgcgtacacagcttggtgttcacagacatctccacaaagagcgctgcgcgcgcgtg 720  
 Db 689 cgtgcgcgtacacagcttggtgttcacagacatctccacaaagagcgctgcgcgcgcgtg 748

CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
CC PRO1187, PRO1281, PRO1303, PRO1309, PRO1317, PRO1710, PRO2094,  
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
growth. The PRO polypeptides and nucleotides are useful in the  
CC treatment, diagnosis and prevention of cancer. The antibodies and other  
CC anti-tumour compounds may be used to treat various conditions, including  
CC those characterised by overexpression and/or activation of the amplified  
CC PRO genes. Exemplary conditions or disorders to be treated with such  
CC antibodies and other compounds include benign or malignant tumours  
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,  
CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic  
CC leukemias, sarcomas, glioblastomas, and various head and neck tumours),  
CC glioma, astrocytoma, hypochromic and other disorders such as neuronal,  
CC epithelial, stromal and blastocoele disorders, and inflammatory,  
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR  
CC primers and hybridisation probes used in the isolation of the human PRO  
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human  
CC PRO polynucleotide and protein sequences given in the exemplification of  
CC the present invention.

XX Sequence 1114 BP: 188 A: 379 C: 356 G: 191 T: 0 other:

Query Match 94.6%; Score 1019; DB 21; Length 1114;  
Best Local Similarity 100.0%; Pred. No. 1.2e-179;  
Matches 1019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctctcctgtctcagcaagacacgagcgctgagggcgccctgctgctg 60  
DB 77 gctctcctgtctcagcaagacacgagcgctgagggcgccctgctgctg 136  
QY 61 tgcctgtgtgtgctgctgctgctgctgctgctgctgctgctgctg 120  
DB 137 tgcctgtgtgtgctgctgctgctgctgctgctgctgctgctgctg 196  
QY 121 acacccac 180  
DB 197 acacccac 256  
QY 181 ccccccagac 240  
DB 257 ccccccagac 316  
QY 241 tgcac 300  
DB 317 tgcac 376  
QY 301 gctcctgtgagagcgctgagagagcgctgagagagcgctgagagag 360  
DB 377 gctcctgtgagagcgctgagagagcgctgagagagcgctgagagag 436  
QY 361 tgcagctgagagcgctgagagagcgctgagagagcgctgagagag 420  
DB 437 tgcagctgagagcgctgagagagcgctgagagagcgctgagagag 496  
QY 421 ccaactgtgtgctgctgctgctgctgctgctgctgctgctgctgctg 480  
DB 497 ccaactgtgtgctgctgctgctgctgctgctgctgctgctgctgctg 556  
QY 481 tgcacccac 540  
DB 557 tgcacccac 616  
QY 541 aactgacagcgccctgtgagcgctgagcgctgagcgctgagcgctg 600  
DB 617 aactgacagcgccctgtgagcgctgagcgctgagcgctgagcgctg 676  
QY 601 tgcacagctgacgtgctgctgctgctgctgctgctgctgctgctgctg 660  
DB 677 tgcacagctgacgtgctgctgctgctgctgctgctgctgctgctgctg 736

QY 661 cgtgcctgacacgacttctgcttccagagacatccatcaagaagctgcagcgctg 720  
DB 737 cgtgcctgacacgacttctgcttccagagacatccatcaagaagctgcagcgctg 796  
QY 721 ctgagagccctcagagcccccagagagctgagctgagctgagctgagctgagctg 780  
DB 797 ctgagagccctcagagcccccagagagctgagctgagctgagctgagctgagctg 856  
QY 781 ttgagctgaagctgctgctgctgctgctgctgctgctgctgctgctgctgctg 840  
DB 857 ttgagctgaagctgctgctgctgctgctgctgctgctgctgctgctgctgctg 916  
QY 841 ctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 900  
DB 917 ctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 976  
QY 901 cgtgagagcttctcctcctgctgctgctgctgctgctgctgctgctgctgctg 960  
DB 977 cgtgagagcttctcctcctgctgctgctgctgctgctgctgctgctgctgctg 1036  
QY 961 gcacccacacttgacatgaagaagcttctttaaataagaagaatgagttcttaa 1019  
DB 1037 gcacccacacttgacatgaagaagcttctttaaataagaagaatgagttcttaa 1095

RESULT 10  
AAC58581 standard; CDNA: 1114 BP.  
ID AAC58581  
AC AAC58581:  
DT 29-JAN-2001 (first entry)  
XX Human PRO212 protein UNQ166 encoding CDNA SEQ ID NO:13.  
XX Human  
XX Human: immune related disease; diagnosis; antiinflammatory; cardiant;  
XX dermatological; antiarthritic; antirheumatic; immunosuppressive;  
XX haemostatic; antithyroid; antidiabetic; neutrotropic; neuroprotective;  
XX antianaemic; hepatotropic; virucide; antiparasitic; antiallergic;  
XX antistomatitic; systemic lupus erythematosus; rheumatoid arthritis;  
XX osteoarthritis; spondyloarthropathy; systemic sclerosis; thyroiditis;  
XX idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
XX autoimmune thrombocytopenia; autoimmune haemolytic anaemia; diabetes mellitus;  
XX autoimmune vasculitis; autoimmune renal disease;  
XX demyelinating disease; hepatobiliary disease; Whipple's disease;  
XX inflammatory bowel disease; gluten-sensitive enteropathy;  
XX autoimmune disease; immune-mediated skin disease; allergic disease;  
XX immunological disease; transplantation associated disease;  
XX graft rejection; graft-versus-host-disease; SS.  
OS Homo sapiens.  
XX  
XX WO200053758-A2.  
XX 14-SEP-2000.  
XX  
XX  
XX 02-MAR-2000; 2000MO-US05841.  
XX  
XX 08-MAR-1999; 99MO-US05028.  
XX 10-MAR-1999; 99US-0123618.  
XX 12-MAR-1999; 99US-0123957.  
XX 23-MAR-1999; 99US-0125775.  
XX 12-APR-1999; 99US-0128849.  
XX 20-APR-1999; 99MO-US08615.  
XX 28-APR-1999; 99US-0131445.  
XX 04-MAY-1999; 99US-0132371.  
XX 14-MAY-1999; 99US-0134287.  
XX 02-JUN-1999; 99MO-US12252.  
XX 23-JUN-1999; 99MO-US141037.  
XX 20-JUL-1999; 99US-0144758.  
XX 26-JUL-1999; 99US-0145698.  
XX 28-JUL-1999; 99US-0146222.  
XX 01-SEP-1999; 99MO-US20111.









XX WO200073452-A2.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PF 02-JUN-2000; 2000WO-US15264.  
 XX  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144722.  
 PR 20-JUL-1999; 99US-0144728.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99US-0170262.  
 PR 09-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 2000WO-US00219.  
 PR 05-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 XX  
 XX (GENTH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
 PI Wood WI;  
 DR P-PSDB; AAB50903.  
 XX  
 DR WPI: 2001-025253/03.  
 XX  
 PS Claim 48; Fig 3; 218bp; English.

Thirty three nucleic acids encoding PRO polypeptides which are useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

XX The present sequence is one of thirty three nucleic acids encoding PRO polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis), inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases (such as bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis), allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunological diseases of the lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis), transplantation associated diseases including graft rejection and graft-versus-host diseases.

Sequence 1114 BP; 188 A; 379 C; 356 G; 191 T; 0 other;

Query Match	94.6%	Score 1019	DB 22	Length 1114
Best Local Similarity	100.0%	Pred. No. 1.2e-179		
Matches 1019	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 1 gctctccctgctccagcaagagcaatgagggcgctgaggggagggcgctgctgctg 60				
Db 77 gctctccctgctccagcaagagcaatgagggcgctgaggggagggcgctgctgctg 136				
QY 61 tgcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 120				
Db 137 tgcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 196				
QY 121 acacccacctacccttgctgctgctgctgctgctgctgctgctgctgctgctgctg 180				
Db 197 acacccacctacccttgctgctgctgctgctgctgctgctgctgctgctgctgctg 256				
QY 181 ccccccagcactcttgctgctgctgctgctgctgctgctgctgctgctgctgctg 240				
Db 257 ccccccagcactcttgctgctgctgctgctgctgctgctgctgctgctgctgctg 316				
QY 241 tctccacgcgcgcactaccagcaatctggaactctggaacgctgctgctgctgctg 300				
Db 317 tctccacgcgcgcactaccagcaatctggaactctggaacgctgctgctgctgctg 376				
QY 301 gctctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 360				
Db 377 gctctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 436				
QY 361 tgcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 420				
Db 437 tgcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 496				
QY 421 ccaactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 480				
Db 497 ccaactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 556				
QY 481 tgcctcccgagcactctctccagcagagctcagctcagctcagctcagctcagctcag 540				
Db 557 tgcctcccgagcactctctccagcagagctcagctcagctcagctcagctcagctcag 616				
QY 541 aactgcaagcctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 600				
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QY 661 cgtgacgctgactgactgctgctgctgctgctgctgctgctgctgctgctgctgctg 720				
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QY 721 cgtgacgctgactgactgctgctgctgctgctgctgctgctgctgctgctgctgctg 780				
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XX AAX07226;  
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XX 21-MAY-1999 (first entry)  
XX  
XX Human tumour necrosis factor receptor ZTNFR-5 cDNA.  
DE  
XX ZTNFR-5; tumour necrosis factor receptor; TNFR; human;  
KM cell maturation; bone cell regulation; ss.  
XX  
XX Homo sapiens.  
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XX Key location/Qualifiers  
FH 183..1085  
FT CDS  
FT sig\_peptide 183..251  
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FT mat\_peptide 252..1082  
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FT Claim 13(b)"  
FT misc\_feature 183..764  
FT /tag= d  
FT /note= "this region is specifically claimed in  
FT Claim 13(c)"  
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FT Claim 13(d)"  
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FT Claim 13(a)"  
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XX MO904001-A1.  
XX  
XX 28-JAN-1999.  
XX  
XX 21-JUL-1998; 98WO-US15072.  
XX  
XX 21-JUL-1997; 97US-0053203.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Farrah TM;  
XX  
XX WPI: 1999-132245/11.  
DR P-PSDB; AAW97749.  
XX  
XX Novel tumour necrosis factor receptor ZTNFR5 - useful for  
PT regulating maturation of TNF-ligand bearing cells  
XX  
XX Claim 13(e); Page 82-85; 109pp; English.  
XX  
XX This DNA sequence codes for a new, secreted tumour necrosis factor  
CC receptor (see AAW97749), designated ZTNFR-5. Novel ZTNFR-5 encoding  
CC polynucleotides and polypeptides were initially identified by  
CC querying an expressed sequence tag (EST) database for sequences  
CC homologous to conserved motifs within the TNF receptor family.  
CC Based on this search, a contig of 16 ESTs was constructed. ZTNFR-5  
CC polypeptides comprise 4 cysteine-rich repeats (see AAW97750-55) that  
CC are homologous to other TNF receptors. In particular the soluble,  
CC secreted TNF receptor osteoprotegerin. ZTNFR-5 polypeptide can be  
CC prepared by recombinant methods. The polypeptide, especially the  
CC extracellular domain, can be used to generate a soluble variant of  
CC ZTNFR-5. The polypeptides and nucleic acids can be used to screen  
CC for agonists and antagonists of ZTNFR-5. The polypeptides can be  
CC used in bone cell regulation and to regulate the maturation of TNF

CC ligand-bearing cells such as T- or B-cells, lymphocytes, peripheral  
CC blood mononuclear cells, polymorphonuclear leukocytes, fibroblasts  
CC or haematopoietic cells.  
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XX Sequence 1205 BP; 205 A; 407 C; 386 G; 207 T; 0 other;  
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Best Local Similarity 100.0%; Pred. No. 1.2e-179;  
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DB 159 gctctccctgctccagcaagaccatgagggcgctggaggccagcgtctgctgctg 218  
QY 61 tgcctggtgttgccgctgctgctgctgctgctgctgctgctgctgctgctgctg 120  
DB 219 tgcctggtgttgccgctgctgctgctgctgctgctgctgctgctgctgctgctg 278  
QY 121 acacccactacccttgccgctgctgctgctgctgctgctgctgctgctgctgctgctg 180  
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QY 361 tgcgcgtgctgcgacccgctctctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 420  
DB 519 tgcgcgtgctgcgacccgctctctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 578  
QY 421 ccaactggtgctggcgcgatgtgcccggcgaccccccagccagacacgcgtgcccgcgcg 480  
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DB 879 cttgcaagcctcagagcccgagggcgctgggtctcgaacacaaaggcgcgcgccg 938  
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DB 999 ctgtgagctgctgcaagcgagcgctgctgctgctgctgctgctgctgctgctgctgctg 1058  
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Db 1059 cgtgagcgcttcctccctgctgacatgacccctgcccccttattatctacacctgt 1118  
Qy 961 gcacccacactgacatgaaagagcttttttaataataaagaaatgagttcttaaa 1019  
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RESULT 15

AAK32744  
ID AAK32744 standard; DNA; 1114 BP.

AC AAK32744;

DT 24-JUN-1999 (first entry)

DE Human DCR3 polypeptide encoding DNA.

KW DCR3 polypeptide; tumour necrosis factor receptor; TNFR; Fas ligand;  
KW apoptosis; T cell mediated immune response; allergy; asthma; cancer;  
KW rheumatoid arthritis; Crohn's disease; guest vs. host disease; human;  
KW gene therapy; ss.

OS Homo sapiens.

PN WO914330-A1.

PD 25-MAR-1999.

PF 18-SEP-1998; 98WO-US19661.

PR 30-JUL-1998; 98US-0094640.

PR 18-SEP-1997; 97US-0059288.

PA (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Botstein D, Dodge KH, Goddard A, Gurney AL;  
PI Kim KJ, Lawrence DA, Pittl R, Roy MA, Tumas DB;  
PI Wood WI;

DR MPI: 1999-244032/20.

DR P-PSDB; AAY06817.

PT DCR3 polypeptide related to tumor necrosis factor receptor

PS Examples; Fig 2; 88pp: English.

CC This DNA encodes a human DCR3 polypeptide, a homologue of tumour necrosis  
CC factor receptor (TNFR) polypeptide. Host cells containing a vector  
CC comprising the DCR3 nucleic acid can be used for the recombinant  
CC expression of the protein. DCR3 binds to Fas ligand, so it (or its  
CC chimeras) are useful for modulating apoptosis in mammalian cells, also  
CC other Fas-ligand induced activities, particularly to inhibit T cell  
CC mediated immune responses, e.g. in treatment of allergy, asthma,  
CC rheumatoid arthritis, Crohn's disease, guest vs. host disease etc. DCR3  
CC may also be used to identify specific binding proteins, potential  
CC inhibitors. Antibodies against DCR3 are used to treat cancer,  
CC specifically of the lung and colon, also in diagnosis and for affinity  
CC purification of the protein. Detecting mutations in the gene for DCR3 is  
CC also used to diagnose cancer, or predisposition to it. DCR3 nucleic acid  
CC is useful as hybridization probe to detect genomic or related sequences;  
CC for chromosome and gene mapping; as source of antisense sequences; for  
CC expression of recombinant DCR3 and to generate transgenic animals (for  
CC development and screening of therapeutic agents), also for in vivo or  
CC ex vivo gene therapy.

SO Sequence 1114 BP; 188 A; 378 C; 356 G; 191 T; 1 other;

Query Match 94.5%; Score 1018; DB 20; Length 1114;  
Best Local Similarity 99.9%; Pred. No. 1.8e-179;  
Matches 1018; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gcttcctgctccagcaagacatgagcgctggaaggcgccagcgctgctgctg 60

Db 77 gcttcctgctccagcaagacatgagcgctggaaggcgccagcgctgctgctg 136  
Qy 61 tgcctgtgttgagctgcctgcctgctgctgcctgctgcctgctgcctgctgcctg 120  
Db 137 tgcctgtgttgagctgcctgcctgctgctgcctgctgcctgctgcctgctgcctg 196  
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science 248, 119-1023, 1990  
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and  
A:Reference number: A35356; MUID:90260639  
A:Accession: A35356  
A>Status: Preliminary  
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A:Residues: 1-461 <SM>  
A:Cross-references: GB:M52315; NID:q189185; PIDN:AAA59929.1; PID:q189186  
R:Kohn, T.; Brenet, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires  
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur  
A:Reference number: A36475; MUID:91045391  
A:Accession: A36475  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195, 'R', 197-461 <ROH>  
A:Cross-references: GB:M55994; GB:M48549; NID:q339757; PIDN:AAA6755.1; PID:q339758  
R:Demblé, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.  
Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,  
A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
A>Status: Preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 23-461 <DEM>  
A:Cross-references: GB:G563368; NID:q235648; PIDN:AAI18824.1; PID:q235649  
A>Note: sequences extracted from NCBI backbone (NCBIIN:63368, NCIP:63371)  
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstr  
A:Reference number: A36007; MUID:90349572  
A:Accession: A36007  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HE>  
A:Cross-references: GB:M58857; NID:q339751; PIDN:AAA63262.1; PID:q339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.  
J. Biol. Chem. 265, 20131-20138, 1990  
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec  
A:Reference number: A23566; MUID:91056048  
A:Accession: A23566  
A>Status: Preliminary  
A:Molecule type: protein  
A:Residues: 23-40;55-69;136-141;300-306 <LOE>  
R:Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A:Reference number: A35010; MUID:9010215  
A:Accession: B35010  
A>Status: Preliminary  
A:Molecule type: protein  
A:Residues: 27-31 <ENG>  
R:Kuhnert, P.; Kemper, O.; Wallach, D.  
Gene 150, 381-386, 1994  
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of  
A:Reference number: I38094; MUID:95121934  
A:Accession: I38094  
A>Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-37 <RES>  
A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CA56324.1; PID:g825701  
C:Genetics:  
A:Gene: GDB:TNFR2  
A:Cross-references: GDB:125914; OMIM:191191  
A:Map position: 1p36.2-1p36.2  
A:Introns: 26/3  
A>Note: the list of introns is incomplete  
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
E:1-32/Domain: signal sequence; status predicted <SIG>  
E:23-416/Product: tumor necrosis factor receptor 2; status experimental <MAT>  
E:40-76/Domain: NGF receptor repeat homology <NG1>  
E:78-119/Domain: NGF receptor repeat homology <NG2>









Mon Nov 5 08:22:34 2001

us-09-006-352-1.rpr

Page 6

A:Experimental source: strain India-1967, ssp. major, isolate ind3  
R:Kolyhalov, A.A.; Blinov, V.M.; Gytocov, V.V.; Pozdnyakov, S.G.; Chuzhikov, V.E.; Frolo  
submitted to the EMBL Data Library, April 1992  
A:Description: Nucleotide sequence analysis of the region of Varicella virus Xhol F O H P  
A:Accession number: S46868  
A:Reference number: S46868  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <KOL>  
A:Cross-references: EMBL:M67117; NID:G516428; PIDN:CAA47540.1; PID:G516449  
A:Experimental source: strain India-1967, isolate ind3  
R:Shchepkinov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.  
FEBS Lett. 319, 80-83, 1993  
A:Title: Genes of varicella and vaccinia viruses necessary to overcome the host protective  
A:Reference number: S32385; MUID:93202281  
A:Accession: S32385  
A:Molecule type: DNA  
A:Residues: 31-168 <SHC>  
A:Cross-references: EMBL:X69198  
A:Experimental source: strain India-1967, ssp. major  
A:Genetics: R  
A:Gene: GAr  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
F:32-66/Domain: NGF receptor repeat homology <NGF>  
F:66-109/Domain: NGF receptor repeat homology <NG2>  
F:110-151/Domain: NGF receptor repeat homology <NG3>

[illegible]

US-09-006-352-1 x D36858

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[illegible]

seq\_name: p1r2:728623

C:Idate: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
C:Accession: T28623  
R:Masung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au-  
Nature 366, 748-751, 1993  
A:Title: Potential virulence determinants in terminal regions of varicella smallpox viru-  
A:Reference number: Z20488; MUID:94088747  
A:Accession: T28623  
A:Status: preliminary; translated from GB/EMBL/DBDB  
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A:Residues: 1348 <MAS>  
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A:Experimental source: strain Bangladesh 1975  
A:Superfamily: myxoma virus B2 protein, NGF receptor repeat homology

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US-09-006-352-1 X T28623

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[illegible]





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|||||
575 CAGGCTCTCTCCCAATGACACACCTGTGCACACAGCTGCATGCGCTTCCGCC 624
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154 roLaserAsnSerLeuAspThrValCysGlnAspArgSer.....Leu 168
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625 CTCAGCACACAGGTACCAAGAG.....CTGAGAGATGTGA 659
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710 TGCAGCGGCTGCTGCAGGCGCTGCAGGCGCCGGA.....G 744
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seq\_name: pIrr2:I37552

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C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C:Accession: I37552  
R:Latza, U.; Durkop, H.; Schultze, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat  
Eur. J. Immunol. 24, 677-683, 1994  
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment  
A:Reference number: I37552; MIMD:94170844  
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C:Superfamily: CD27 antigen; NGF receptor repeat homology

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Align seg 1/1 to: I37552 from: 1 to: 277

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11 GlyProCysAlaAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuValTh 27
|||||
90 GCGCGTGGCGCTGTACGCGGAGTGGCAGAAACACCACTACCTACCTGGC 139
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27 rGlyLeuHisCysVal.....GlyAspThrTrpProsera 39
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140 GGGAGCAGAGACAGAGGGAGCGGCTGTGTGCGCCAGTGGCCGCCAGGC 189
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39 snAspArg.....CysCysHisGluCysArgProGly 49
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190 ACCTTTGTGACGCGCGCTGCGCGGAGACAGCCCAAGAGAGTGGCGCC 239
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50 AsnGlyMetValSerArgCysSerArgSerGlnAsnThrValCysArgPr 66
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240 GTGTTCACCGCGGCACCTACACGAGTTCTGGAAGTAC.....CTGAGC 283
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seq\_name: pIrr2:F75518

seq\_documentation\_block:

hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
C:Accession: F75518  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MIMD:20036896  
A:Accession: F75518

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66 ocYsLysProGlyProGlyPheThrAsnAspValValSerSerLysProCysLysP 83
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284 GTCGCGGCTACTGCAGACCTCTGCGGGAGCGGAGAGAGAGAGAGAGAG 333
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83 rocYsThrTrpCysAsnLeuArgSerGly.....SerGluArgLysGln 97
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334 GCTTGCACGCGCCACCCACACACCGTGCCTGCGCTGCGCGCGAGCGCTTCT 383
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98 LeuYsThrAlaThrGlnAlaPThrValCysArgCysArgAlaGly..... 112
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384 GCGGCACGCTGTTTCTGCTTGGACACACGATTCGTCACCTGGTGGCG 433
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434 GCGTATTTGCCCCGGGCGACCCCGCAAGACAGCAATGCGACCGCTGC 483
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123 .....ValAspCysAlaProCys 128
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484 CCGCCAGCAGCTTCTCTACGCGAGCTCAGCTCAGCTCAGAGTGCAGCC 533
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129 ProProGlyHisPhe.....SerProGlyAspAsnGlnAlaCysLysPr 143
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534 CCACCGCAGCTGCAGGCGCTGGGCGCTGGCGCTCAATGTGCCAGGCTCTT 583
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143 oTrpThrAsnCysThrLeuAlaGlyLysHisThrLeuGlnProAlaSerA 160
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584 CTTCCCATGACACCGCTGTGCACAGC.....TGCACGTGCTGCC 624
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160 snSerSerAspAlaIleCysGlnAspArgAspProProAlaThrGlnPro 176
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177 GlnGluThrGlnGlyProProAla..ArgProIleThrValGlnProThrG 193
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675 CTTTGTGCGCTTCCAGCAGATCTCCATGACAGAGCTGCAGCGGCTGTGC 724
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193 IuAlaTrp...ProArgThrSer..... 199
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725 AGGCGCTGAGAGCGCGGAGGCTGGGCTCCGACACAGAGGCGGCGCGC 774
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227 .....LeuLeuGlyProLeuAlaI 233
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A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-839 <WHI>  
 A:Cross-references: GB:AE001904; GB:AE000513; NID:g6458129; PID:AAF10038.1; PID:g645814  
 A:Experimental source: strain R1  
 C:Genetics:  
 A:Gene: DR0458  
 A:Map position: 1  
 C:Superfamily: herpesvirus immediate-early protein IE110; RING finger homology

alignment\_scores:  
 Quality: 224.00 Length: 362  
 Ratio: 1.258 Gaps: 14  
 Percent Similarity: 49.171 Percent Identity: 30.110

alignment\_block:  
 US-09-006-352-1 x F75518 ..

Align seg 1/1 to: F75518 from: 1 to: 839

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320  AlapromserserAlaAlaAlaProsnoluproAlaseroluprova 336
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53  CGCTGCTGTGCTGCTGTGGCGCTGCCCTGCTCCCT 86
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336  lAlaGlyArgProGlyThrAlaAlaSerSerProGlySerAlaSerPro 353
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87  .....GCTGCCGCTGCCGC 101
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137  .....GGCGGACGACAGACAGGAGGCGGCTGCTGCCGCGCAG 177
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178  TGCCCCCGACGACCTTG.....TGACGCGCC 206
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402  olleProAlaThrProIleProAlaThrProAlaGlyArgSerSerGlyG 419
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207  GTGCCCGCGAGACGCCACGAGCT.....GTGCCGCGCTGC 244
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419  luserAlaGlyThrAlaAlaAlaAlaArgProasmlAlaAlaProAlaProva 435
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245  CACCGGCGCACACGAGCTTTCGGAACACTGAGAGCGCTGCCGCTAC 294
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436  SerGluAspArgSerAspValSerGlyluphrProArgArglupAlaPr 452
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295  TCGAACGCTCTGCGGGGAGCGTGAGAGAGCGGCTTCCACGC 344
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452  oAlaGlySerSerProvalAlaAlaAlaSerProAlaArgGlyAlaSerSerA 469
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345  CACCCCAACAGCTGCTGCCCTGCCGACCGGCTTCTTGGGACGCTG 394
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469  lProSerSerAlaProAlaAlaAlaValPro.....SerArgAlaPro 483
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395  GTTCTGCTTGGAGACGACATGTCACCTGTGCGCGCTGATGTC 444
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484  ValSerGlyGlySerValSer.....AlaProAlaArgThrAlaPr 496
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445  CCGGCGACCC.....CCAG 458
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496  oThrAlaProvalAlaGluGluGlylupAlaProvalSerProserAlaA 513
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459  CCGAAGACGAGTGGCAGCGCTGCCCGCCAGCACCTTCTCAGACAGA 508
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513  lAlaAlaProArgGlyGlyAlaSerSerAlaAlaAlaProserAlaProAla 529
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561  lAlaGlyAlaSerGlyGlyGlyGlyGly.....Val 571
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659  AGCGTCCGTCATCGACTTGTGCTTCCAGGACATCTCATCAGAG 708
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572  Ser..AlaArgProSerGlylupThrProSerGlylupThrProAlaSerA 588
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709  CTGCAGCGGCTGCTGCAGGCGCTCCAGGCGCCGAGGCTGGGCTCCAGC 758
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588  lAlaProAlaAlaAlaGlyArgProAlaGlyGlyGlySerGlySerGly 604
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
759  ACCAAGGCGGCGCGCGCGCTTGCACGTGAGCTGCGGCGGCTCA 808
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
605  ThrSerGlySerGlySerGlySerGlySerGlySerGlySerGlySerGly 620
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835  GCGCTGCTGCTGCGGCTGCTGCAGGCGGCTGCGGCGGCGGAGATGCCG 884
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637  lylGlySerGlyAlaGlyAlaGlyAlaGlyAlaGlylupThrGlyGly 650
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
885  GCTGAGCGGAGGCGCTGAGCGGCTGCTCCCTCC 917
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
651  ThrGlyAlaGlylupThrProserAlaSerArgPro 661
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seq\_name: p1r2:744768  
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 antifreeze glycoprotein AFgp polypeptide precursor [Imported] - Boreogadus saida  
 C:Species: Boreogadus saida  
 C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
 R:Accession: T44768  
 R:Chem. L.: DeVries, A.L.; Cheng, C.H.C.  
 Proc. Natl. Acad. Sci. U.S.A. 94, 3817-3822, 1997  
 A:Title: Convergent evolution of antifreeze glycoproteins in Antarctic notothenioid f  
 A:Reference number: 222834; MUID:97268653  
 A:Accession: T44768  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
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alignment\_block:  
 US-09-006-352-1 x T44768 ..

Align seg 1/1 to: T44768 from: 1 to: 507

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1  GCTTCCTGCTCCAGACAGCATGAGGCGCTGGAGGGCCAGGCT 50
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51  GTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 100
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130  gAlaAlaThrProAlaThrAlaAlaAlaThrProAlaThrAlaAlaThrPro 147
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Mon Nov 5 08:22:34 2001

179 ProValAsnAspThrSerCysThrThrThrAlaGly 190

us-09-006-352-1.rpt

Page 12

OM of: US-09-006-352-1 to: SwissProt\_39.\* out\_format : pfs

Date: Oct 31, 2001 12:38 PM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

#### Command line parameters:

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-MODEL=frame+12p.model -DEV=x1h  
-O=/cgn2_1/USPRO_spool/US09006352/runat_30102001_104618_3398/app-query.fasta_1.1150  
-DB=SwissProt_39 -OFMT=fastan -SUFFIX=rs -GAPO=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000  
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELDP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blissum62  
-THR_MAX=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pcr  
-THR_RAN=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NORMEXT -MINLEN=0 -MAXLEN=200000000  
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-DEV=TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1
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#### Search information block:

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Query: US-09-006-352-1  
Query length: 1077  
Database: SwissProt_39.*  
Database sequences: 93435  
Database length: 3425486  
Search time (sec): 27.95000
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score_list:  
Sequence      Strd Orig      Zscore  EScore Len  Documentation  
SwissProt_39:TNR2_HUMAN + 357.00 317.24 1.1e-10 461 | P20333 homo sapiens (human).  
SwissProt_39:TNR2_MOUSE + 340.00 302.54 6.9e-10 474 | P25119 mus musculus (mouse).  
SwissProt_39:TNRC_HUMAN + 315.00 281.70 1.1e-08 435 | P36841 homo sapiens (human).  
SwissProt_39:TNRC_MOUSE + 290.00 260.63 1.7e-07 415 | P50284 mus musculus (mouse).  
SwissProt_39:VC22_VARV + 262.50 238.20 3.6e-06 349 | P34015 variola virus. protei  
SwissProt_39:CD30_HUMAN + 241.00 216.50 3.4e-05 595 | P28908 homo sapiens (human).  
SwissProt_39:VT2_SEPKA + 236.50 212.42 6.3e-05 325 | P25943 shope fibroma virus (S  
SwissProt_39:OX40_RAT + 230.50 212.42 0.0001 271 | P15725 rattus norvegicus (rat).  
SwissProt_39:OX40_HUMAN + 230.00 211.85 0.0001 277 | P43489 homo sapiens (human).  
SwissProt_39:VT2_MXVL + 215.50 189.44 0.0006 326 | P29825 myxoma virus (strain 1  
SwissProt_39:T2D3_HUMAN + 213.50 189.27 0.0006 1083 | P00268 homo sapiens (human).  
SwissProt_39:CD40_HUMAN + 211.00 195.61 0.0011 277 | P25942 mus musculus (human).  
SwissProt_39:OX40_MOUSE + 210.00 194.87 0.0012 272 | P47741 mus musculus (mouse).  
SwissProt_39:CD40_MOUSE + 203.00 188.51 0.0026 289 | P27512 mus musculus (mouse).  
SwissProt_39:CD40_BOVIN + 202.00 188.10 0.0029 269 | P28203 bos taurus (bovine).  
SwissProt_39:NGFR_HUMAN + 186.50 173.69 0.0116 427 | P34013 homo sapiens (human).  
SwissProt_39:SPD2_NBPCL + 186.00 169.16 0.0141 627 | P46804 nephila claviipes (oth  
SwissProt_39:ICP0_HSV1 + 181.00 167.30 0.0264 425 | P07174 rattus norvegicus (rat).  
SwissProt_39:ICP0_HSV1 + 180.50 163.14 0.0247 775 | P08393 herpes simplex virus  
SwissProt_39:SPD2_NBPCL + 180.00 164.03 0.0272 627 | P46804 nephila claviipes (oth  
SwissProt_39:T2D3_HUMAN + 180.00 160.63 0.0244 1083 | P00268 homo sapiens (human).  
SwissProt_39:YH1L_EBV + 179.50 163.28 0.0285 660 | P03181 Epstein-Barr virus (str  
SwissProt_39:ICP0_HSV1 + 179.00 161.86 0.0291 775 | P08393 herpes simplex virus  
SwissProt_39:NGFR_HUMAN + 177.50 161.58 0.0354 660 | P03181 Epstein-Barr virus (str  
SwissProt_39:NGFR_HUMAN + 176.00 163.16 0.0458 416 | P18519 gallus gallus (chick)  
SwissProt_39:41B8_HUMAN + 174.00 164.50 0.0630 255 | P07011 homo sapiens (human).  
SwissProt_39:TEBK_HUMAN + 171.50 164.81 0.0468 4289 | P22105 homo sapiens (human).  
SwissProt_39:CA11_HUMAN + 170.00 151.06 0.0615 1464 | P02452 homo sapiens (human).  
SwissProt_39:CA11_CHICK + 170.00 150.26 0.0687 1453 | P02457 gallus gallus (chick)  
SwissProt_39:YK82_MVCTV + 167.50 152.48 0.1042 721 | O10690 mycobacterium tuber  
SwissProt_39:FASA_PIG + 167.00 156.87 0.1287 332 | P07772 sus scrofa (pig). fast  
SwissProt_39:CA11_CANFA + 166.50 147.23 0.1008 1460 | P09517 canis familiaris (d  
SwissProt_39:NTC3_MOUSE + 166.00 144.36 0.0918 2318 | P061982 mus musculus (mouse).  
SwissProt_39:ICP0_HSV2 + 166.00 150.36 0.1195 825 | P28284 herpes simplex virus  
SwissProt_39:INME_MOUSE + 166.00 147.42 0.1086 1323 | P003391 mus musculus (mouse).  
SwissProt_39:ICP4_HSV1 + 164.50 146.26 0.1285 1298 | P08392 herpes simplex virus  
SwissProt_39:IE18_PVKA + 164.50 145.58 0.1257 1446 | P13479 pseudorabies virus  
SwissProt_39:LMAS_MOUSE + 164.50 139.85 0.1043 3635 | P06100 mus musculus (mouse).  
SwissProt_39:CA44_HUMAN + 164.00 144.19 0.1287 1690 | P53420 homo sapiens (human).
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DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR  
DE BLINDING PROTEIN 2) (TPST1) (P80) (TNF-R2) (P75) (CD120b) (ETANRECEPT).  
GN TNFRSF10 or TNFR2 or TNFR.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP MEDLINE=90260639; PubMed=2160731;  
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
RT Power S.K., Cosman D., Goodwin R.G.;  
RT "A receptor for tumor necrosis factor defines an unusual family of  
RT cellular and viral proteins.";  
RL Science 248:1019-1023(1990).  
RN [2]  
RP MEDLINE=90260639; PubMed=2172983;  
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
RT Hele K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
RT "A second tumor necrosis factor receptor gene product can shed a  
RT naturally occurring tumor necrosis factor inhibitor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
RN [3]  
RP MEDLINE=9629745; PubMed=8661109;  
RA Bellinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
RT Lepallier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;  
RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
RL Genomics 35:94-100(1996).  
RN [4]  
RP MEDLINE=90349572; PubMed=216946;  
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
RT Ringold G.M.;  
RT "Complementary DNA cloning of a receptor for tumor necrosis factor  
RT and demonstration of a shed form of the receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
RN [5]  
RP MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RT "Two tumor necrosis factor-binding proteins purified from human  
RT urine. Evidence for immunological cross-reactivity with cell surface  
RT tumor necrosis factor receptors.";  
RL J. Biol. Chem. 265:1531-1536(1990).  
RN [6]  
RP MEDLINE=91056048; PubMed=2173696;  
RA Loetscher H., Schaefer E.J., Lohm H.-W., Pan Y.-C.E., Lesslauer W.,  
RT Brockhaus M.;  
RT "Purification and partial amino acid sequence analysis of two  
RT distinct tumor necrosis factor receptors from HU60 cells.";  
RL J. Biol. Chem. 265:20131-20138(1990).  
RN [7]  
RP CHARACTERIZATION; PubMed=1328224;  
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
```

RA	Lilpari M.T., Goeddel D.V.;
RZ	"Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT	Characterization of ligand binding, internalization, and receptor phosphorylation."
RL	J. Biol. Chem. 267:21172-21178(1992).
RN	[8]
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.
RX	MEDLINE=99221490; PubMed=10206649;
SA	Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT	"Structural basis for self-association and receptor recognition of human TRAF2."
RL	Nature 398:533-538(1999).
CC	- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	- PTM: PHOSPHORYLATED; MAINTAIN ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES.
CC	- PHARMACOLOGICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND WETTER-AVERTIS). USED TO TREAT MODERATE TO SEVERE RHEUMATOID ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LGAND BINDING PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
CC	- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC	- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC	- WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm"
CC	- DATASAB: NAME=Enbrel; NOTE=Clinical information on Enbrel; WWW="http://www.enbrelinfo.com/"
CC	-----
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CC	-----
DR	EMBL: M32315; AAA59929.1; -;
DR	EMBL: M35857; AAA63262.1; -;
DR	EMBL: U52165; AAC50622.1; -;
DR	EMBL: U52156; AAC50622.1; JOINED.
DR	EMBL: U52157; AAC50622.1; JOINED.
DR	EMBL: U52158; AAC50622.1; JOINED.
DR	EMBL: U52159; AAC50622.1; JOINED.
DR	EMBL: U52160; AAC50622.1; JOINED.
DR	EMBL: U52161; AAC50622.1; JOINED.
DR	EMBL: U52162; AAC50622.1; JOINED.
DR	EMBL: U52163; AAC50622.1; JOINED.
DR	EMBL: U52164; AAC50622.1; JOINED.
DR	EMBL: M55994; AAA67955.1; -;
DR	PIR: A35356; A35356.
DR	PIR: A36007; A36007.
DR	PIR: A36475; A36475.
DR	PIR: B35010; B35010.
DR	PIR: A23666; A23666.
DR	PDB: 1CA9; 12-APR-99.
DR	MMF: 191191; -;
DR	InterPro: IPRO01368; -;
DR	Pfam: PF00030; TNFR_C6; 4.
DR	PROSITE: PS00652; TNFR_NGFR_1; 2.
DR	PROSITE: PS0050; TNFR_NGFR_2; 4.
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Phosphorylation; Pharmaceutical; 3D-structure.
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FT	

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FT DISULEID 54 67 BY SIMILARITY.
FT DISULEID 57 75 BY SIMILARITY.
FT DISULEID 78 93 BY SIMILARITY.
FT DISULEID 96 110 BY SIMILARITY.
FT DISULEID 100 116 BY SIMILARITY.
FT DISULEID 120 128 BY SIMILARITY.
FT DISULEID 134 143 BY SIMILARITY.
FT DISULEID 137 161 BY SIMILARITY.
FT DISULEID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 N-LINKED (GLICNAMC. . .) (POTENTIAL)
FT CARBOHYD 193 193 N-LINKED (GLICNAMC. . .) (POTENTIAL)
FT CONFLICT 141 141 R -> P (IN REF. 4) .
FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3) .
FT CONFLICT 363 363 A -> T (IN REF. 4) .
SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;

Alignment_scores:
Quality: 357.00 Length: 334
Ratio: 1.994 Gaps: 13
Percent Similarity: 53.593 Percent Identity: 29.940

Alignment_block:
US-09-006-352-1 x TNR2_HUMAN ..
Align_sseg 1/1 to: TNR2_HUMAN from: 1 to: 461

10 GCTCCGACGAGGCGCATGAGCGCTGGAGGCGCAGGCTGCTGCT 59
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2 AAlaProValAlaValTrpAlaAlaLeu..AlaValGlyLeuGlnLeuTr 17
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60 GTGCTGTGGTGGTGGCGCTGCGCTGCGCTGCGCGGTACGCG 109
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17 pAlaAlaAlaHisAlaLeuProAla.....G 26
110 GAGTGGCGAGAACACCCGACCTACCCCTGGGCGGAGCAGACAGAGGAG 159
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26 lValAlaIleThrProGlyAlaPro.....GluProGlySer 38
160 .....CGGCTGGCTGCTGCC 173
39 ThrCysArgLeuArgGlyTrpTyrAspGlnThrAlaGlnMeCysCysSe 55
174 CCAAGTCCCCCGAGCGACCTTGTGACGCGCGCGCCGCGCAGACAGCC 223
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55 lTlyCysSerProGlyGlnHisAlaLysValIlePheCysThrLysThrSerA 72
224 CACGAGCGGTGGCGCGCTGCTCCACCGCGGCACCTACACGAGATTGCAAC 273
   ||||| ||||| |||||
72 spThrValCysAspSerCysGlnAspSerThrTyrThrGlnLeuTrpAsn 88
274 TACCTGAGCAGCGTGGCGCTGCTACGACAGCTCTGTGGCGGAGCGAGAGA 323
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69 TrpValProGlyLucyLysSerCysGlySerArgCysSerSerAspGlnVa 105
324 GAGGAGGAGGAGGCTGCGCAGCGCACCGACACGACGAGCGCTGCGCTGGCA 373
   |||||::: ||||| ::::: ||||| |||||
105 lGluThrGlnAlaCysThrArgGlnGlnAsnArgIleCysThrCysArgp 122
374 CGGGCTTTCGGCGACGCTGCT.....TTCGCTTG 405
122 roGlyTrpTrpTrpCysAlaLeuSerLysGlnGlnGlyCysArgLeuGlnCysAla 138
406 GAGCAGCGATCGTGTCCACCTGTGCGCGCGGTGATTTGCCCGGCGACCCC 455
   ::::: ||||| ||||| ||||| |||||
139 ProLeuArgLysCysValProGlyPheGlyValAlaAlaArgProGlyThrGln 155
456 CAGCCAGAAACAGCGATCCACGCGCTGCCCGCCGAGGACCTTTCAGGCA 505
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155 uGlnSerAspValValCysLysProCysAlaArgProGlyThrPheSerAsnTr 172
506 GAGGCTTCAGCTCAAGAGGAGCGAGCGCCACCGACGACAGCGAGCCCTG 555
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172 hrtHrSerThrAspIleCysAlaProHisGlnIleCysAsnValVal 188
556 GGCCTGGCCCTCAATGTCAGGCTCTCTCCATGACACCTGTGAC 605
189 Ala.....IleProGlyAsnAlaSerAlaGspAlaValCysTh 201
606 CAGCTGCACGTGGCTTCCCTCCACAGGAGGACAGAGCTGAGAGT 655
201 rSerThrSer.....ProThrArgSerMetAlaProGlyAlaValHisL 216
656 GTGAGCGTGGCCGTCATGACACTTGTGGCTTCCAGACATCTCATCAG 705
216 euProGlnProVal.....SerThrArgSerGln 225
706 AGGCTGACAGCGGTGCTGTCAGAGCCCTGAGCCCGGAG..... 744
226 HisThrGlnProThrProGlnProSerThrAlaProSerThrSerPheLe 242
745 ...GGCTGGGTCGACACCAAGGCGC.....GGCCGCGCGG 778
242 uLeuProMetGlyProSerProAlaGlnGlySerThrGlyAspPheA 259
779 CCTTGACAGCTAAGCTGCGTGGCGGCTCAGGAGCTCTCTGGGGCGAG 828
259 lAlaProValGlyLeuValGlyAlaThrAlaLeu..... 271
829 GAGCGGCGCTGCTGTGTCGCGCTGTCAGAGCGCTG.....CGCGT 869
272 ...GlyLeuLeuIleIleGlyValValAlaCysValIleMetThrGlnVa 287
870 GCGCAGGATGCGC...GGCTGAGAGCGAGCGCTGACGCGCTTCCTCC 916
287 lLysIleLysProLeuGlyAlaGlnAlaGlyAlaValProHisLeuP 304
917 CT 918
304 TO 304

seq_name: SwissProt_39:TNR2_MOUSE
seq_documentation_block:
ID TNR2_MOUSE STANDARD; PRT; 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9187885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=NOD;
RA Jacob C.O., Liu J.;

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RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-22 FROM N.A.
RC Tissue=Liver;
RA Kissenbergh M., Fellows R., Feldmann M., Chernajovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL: M60469; AAA39752.1; -
DR EMBL: M59378; AAA40463.1; -
DR EMBL: U39488; AAA85021.1; -
DR EMBL: X87128; CAA60618.1; -
DR PIR: B38634; B38634.
DR HSSP: P19436; INCF.
DR MGD: MGI:1314883; Tnfrsf1b.
DR InterPro: IPR001368; -
DR Pfam: PF00020; TNFR_c6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 259 288 POTENTIAL.
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 203 4 X TNFR-CYS.
FT REPEAT 39 77 TNFR-CYS 1.
FT REPEAT 78 119 TNFR-CYS 2.
FT REPEAT 120 164 TNFR-CYS 3.
FT REPEAT 165 203 TNFR-CYS 4.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

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Quality: 340.00 Length: 278
Ratio: 2.152 Gaps: 12
Percent Similarity: 56.835 Percent Identity: 32.014

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52 GlnMetCysAlaIleCysProProGlnGlnValValHisPheCys 68
210 CCGCGGAGACAGCCGACGAGCTGCGCGCTGTCACGCGGCGCACTCA 259
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68 sasnLysThrSerThrValCysAlaAspCysAlaAspCysAlaSerMetYrt 85

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149 AGACAGGGAGGAGCGCTGGTGTGCCCCAGTGGCCCCAGGACGACCTTTGTG 198
38 ..LysAlaGlnAsnLeuScysLeuSerCysProProGlyThrTyrAla 53
199 CAGCGGCGCGTCCCGCCGAGACGCCAGGACGAGCTGGCCGTGTCCACCC 248
54 SerArgLeuScysAspSerLysThrAsnThrGlnGlyThrProCysGlySe 70
249 GCGGCACTACACGAGTTTGGAGATACAGTGGAGCGGCTGGCCGCTACTGCA 298
70 rGlyThrPheThrSerArgAsnAsnHisLeuProAlaCysLeuSerCysA 87
299 ACGTCTCTCGCGGAGAGCGTGGAGAGGACGAGCGGCTGGCCAGCCACC 348
87 snGlyArgCysAsnSerAsnGlnValGlnThrArgSerCysAsnThrThr 103
349 CACACAGCGTGGCTGGCGTGGCCGAGCGGCTTTC..... 384
104 HisAsnArgLecCysGlyCysSerProGlyTyrTyrCysLeuLysG1 120
385 ....GCGCAGCGTGGTTCTGCTGGAGACGACGATGTCACCTGGTG 430
120 ySerSerGlyCysLysAlaCysValSerGlnThrLysCysGlyLecGlyT 137
431 CCGCGCTGATTTGCCCGGAGGACCCCGACGACGACGACGACGACGACG 480
137 yrglyVal...SerGlyHisThrSerValGlyAspValLecCysSerPro 152
481 TGCCCCAGGACGACCTTCTCAGCCAGGCTCCGACGACGACGACGACG 530
153 CysGlyPheGlyThrTyrSerHisThrValSerSerAlaAspLysCysG1 169
531 GCCCAGCGACGACGACGACGACGACGACGACGACGACGACGACGACG 580
169 uProValProAsnAsnThrPheAsnTyrLecAspValGlnLecThrLeuT 186
581 CTTCCTCCCATGACACCCCTGTGACACGACGACGACGACGACGACGAC 630
186 yrrProValAsnAspThrSerCysThrArgThrThrThrThrGlyLeuSer 202
631 ACCAGGAGACGACGACGACGACGACGACGACGACGACGACGACGACG 651
203 GluSerIleLeuThrSerGlu 209
seq_name: SwissProt_39:CD30_HUMAN
seq_documentation_block:
ID CD30_HUMAN STANDARD: PRT: 595 AA.
AC P28908;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD30L RECEPTOR PRECURSOR (LYMPHOCYTE ACTIVATION ANTIGEN CD30) (KI-1
DE ANTIGEN).
OS TNFRSF8 OR CD30.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=92154659; PubMed=1310894;
RA Duerkop H., Latza U., Hummel M., Eitelbach F., Seed B., Stein H.;
RT "Molecular cloning and expression of a new member of the nerve growth
RT factor receptor family that is characteristic for Hodgkin's
RT disease."
RL Cell 68:421-427(1992).
RP [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=95089787; PubMed=7527901;
RA Jung W., Krueger S., Renner C., Gause A., Sahin U., Trumper L.,
RA Pfeundschuh M.;

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RT "Opposite effects of the CD30 ligand are not due to CD30 mutations:
RT results from cDNA cloning and sequence comparison of the CD30 antigen
RT from different sources."
RL Mol. Immunol. 31:1329-1334(1994).
RN [3]
RP SEQUENCE FROM N.A. (VARIANT C30V).
RX MEDLINE=96437016; PubMed=8839832;
RA Horie R., Ito K., Tatewaki M., Nagai M., Aizawa S.,
RA Higashihara M., Ishida T., Inoue J., Takizawa H., Watanabe T.;
RT "A variant CD30 protein lacking extracellular and transmembrane domain
RT is induced in HL-60 by tetradecanoylphorbol acetate and is expressed
RT in alveolar macrophages."
RL Blood 86:2422-2432(1996).
CC - FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD30L. MAY PLAY
CC A ROLE IN THE REGULATION OF CELLULAR GROWTH AND TRANSFORMATION OF
CC ACTIVATED LYMPHOBLASTS. REGULATES GENE EXPRESSION THROUGH
CC ACTIVATION OF NFkB.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - ALTERNATIVE PRODUCTS: A SHORTER CYTOPLASMIC FORM C30V WHICH IS
CC ONLY EXPRESSED IN ALVEOLAR MACROPHAGES IS PRODUCED BY THE USE
CC OF AN ALTERNATIVE INITIATION CODON IN THE SAME READING FRAME.
CC - PTM: PHOSPHORYLATED ON SERINE AND TYROSINE RESIDUES.
CC - DISEASE: MOST SPECIFIC HODGKIN'S DISEASE ASSOCIATED ANTIGEN.
CC - SIMILARITY: CONTAINS A LA-NGER/TNFR-TYPE CYSTEINE-RICH REGION.
CC - DATABASE: NAME=PROV; NOTE=CD guide CD30 entry;
CC WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd30.htm".
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M83556; AAA51947.1; -
DR EMBL: S75766; AAD14186.1; -
DR EMBL: D86042; BAA12973.1; -
DR PIR: A42086; A42086.
DR UISP: P19438; INCF.
DR MIM: 153243; -.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;
KW Phosphorylation; Alternative initiation.
FT SIGNAL 1..18
FT CHAIN 19..595
FT CHAIN 464..595
FT INIT_MET 464..464
FT DOMAIN 19..379
FT TRANSMEM 380..407
FT DOMAIN 408..595
FT DOMAIN 28..325
FT DOMAIN 28..325
FT REPEAT 68..106
FT REPEAT 107..150
FT REPEAT 205..241
FT REPEAT 243..281
FT REPEAT 282..325
FT DOMAIN 347..377
FT CARBOHYD 101..101
FT CARBOHYD 276..276
SQ SEQUENCE 595 AA; 63747 MW; 7A407CC78A6E0BC8 CRC64;

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    Ratio: 1.596
    Percent Similarity: 47.634
    Percent Identity: 28.707
alignment_block:

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US-09-006-352-1 x CD30\_HUMAN ..  
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10 LeuLeuPheLeuGlyAlaLeuAlaPheProGlnAspArgProPheG1 26
   ::::| | | | | | | | | | | | | | | | | | | | |
117 AGAACA.....CCACCTACCTCCGCGCGGAGCGAGACAG 154
   ::::| | | | | | | | | | | | | | | | | | | | |
26 uAspThrCysHisGlyAsnProSerHisTyr.....AspLysA 40
   ::::| | | | | | | | | | | | | | | | | | | | |
155 GAGAGCGGCTGTGTCGCGCCAGTGCAGCCGACCTTTGTGCGAGCG 204
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40 lAlaValArgArgCysTyrArgCysProMetGlyLeuPheProThrGln 56
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205 CCGTGGCCGCGAGACGCGCCGACGCTGT...GGCCGTCGTCACGCGG 251
   || | | | | | | | | | | | | | | | | | | | | |
57 GluCysProGln...ArgProThrAspArgLysGlnCysLeuProAs 72
   || | | | | | | | | | | | | | | | | | | | | |
252 CCACTACAGCGAGTTCTGTGAACTGTGAGAGCTGCGCGCTACTGCAACG 301
   ::::| | | | | | | | | | | | | | | | | | | | |
72 pTyrTyrLeu.....AspGluAlaAspArgCysThrAlaCys...V 85
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302 TCCTGTGCGGAGACGCTGAG...GAGAGCGACGCGGCTTCCACGCGCAC 348
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85 alThrCysSerArgAspAspLeuValGlnLysThrProCysAlaTyrAsn 101
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349 CACACCGTGCCTGCCGCTGCCGCGACGCGCTTCTTCCGCGACGCTGTT 398
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102 SerSerArgValCysLeuLysArgProGlyMetPheCysSerThrSerAl 118
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399 C.....TGCCTTGAGACGACCATCTGCTGCACCTGCTG 430
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118 aValAsnSerCysAlaArgCysPhePheHisSerValCysProAlaGlyM 135
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431 CCGCGCTGATGCCCGGCGACCCGCGACGAGACAGCGAGCTCCGCGG 480
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135 etLeuValLysPheProGlyThrAlaGlnLysAsnThrValCysGluPro 151
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481 TGCCTCCGACGACCTTCTGACGCGCGACGCTGCGCTGACGAGTGC 530
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152 AlAserProGlyVal.SerProAlaCysAlaSerProGlnAsnCysLysG 168
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531 GCGCCACCGGACAGTGCAGCGCGCTGCGCGCTGCGCTGCGCTGCG 580
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168 luoProSerSerGlyThrLeuProGlnAlaLysProThr..... 180
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581 CTTCCTCCGACGACCTGTCGACGAGCTGACAGCTGCTCCCGCTCACG 630
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181 .....ProValSerProAlaThrSerSerAlaSerThrMetProValAr 195
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631 ACCAGCG.....TACAGAGAGCTG..... 649
   ::::| | | | | | | | | | | | | | | | | | | | |
195 gGlyGlyThrArgLeuAlaGlnGluAlaAlaSerLysLeuThrArgAlaP 212.
   ::::| | | | | | | | | | | | | | | | | | | | |
650 .....AGAGTGTGAGCGCTGCCGCTATGACATTGTGCGCTTCC 688
   :: | | | | | | | | | | | | | | | | | | | | |
212 roAspSerProSerSerValGlyArgProSerSerAspProGlyLeuSer 228
   :: | | | | | | | | | | | | | | | | | | | | |
689 AGGACATCTTCATCAAGAGGCTGCAGGCGCTGTGACGCGCTCGAGGCG 738
   || | | | | | | | | | | | | | | | | | | | | |
229 ProThrGlnProCysProGluGlySerGlyAspCysArgLysGlnCysG1 245
   :: | | | | | | | | | | | | | | | | | | | | |
739 CCGGAGCGCTGCGCTGCAGACCAAGAGGCGCGCGCGCGCTTGTGAGCT 788
   :: | | | | | | | | | | | | | | | | | | | | |
245 uProAspTyrTyrLeuAspGluAlaGlyArg.....CysThr. 257
   :: | | | | | | | | | | | | | | | | | | | | |
789 GAGCTGCTGCGCGCTCAGGAGCTCTCGGGGCGCGCAGAGGGGCGCG 838
   :: | | | | | | | | | | | | | | | | | | | | |
258 ...AlaCysValSerCysSerArgAspAspLeuValGlnLysThrProCys 273
   :: | | | | | | | | | | | | | | | | | | | | |
839 TGCTGG.....TGGCGCTGC..... 853

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274 AlAtThrAsnSerSerArgThrCysGluCysArgProGlyMetLeuCysAl 290
   ::::| | | | | | | | | | | | | | | | | | | | |
854 .....TGCAGCGCGCTGCGCG...TGCACGAGCATGC 880
   :: | | | | | | | | | | | | | | | | | | | | |
290 aThrSerAlaThrAsnSerCysAlaArgCysValProTyrProIleCys 306
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seq_name: SwissProt_39:VT2_SFVKA

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seq_documentation_block:
ID VT2_SFVKA STANDARD; PT: 325 AA.
AC P25943;
DT 01-MAY-1992 (rel. 22, Created)
DT 01-MAY-1992 (rel. 22, Last sequence update)
DT 15-JUL-1999 (rel. 38, last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN 72).
GN 72;
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Lepotipoxvirus.
OX NCBI_TaxId=10272;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=87321103; PubMed=2820128;
RA Upton C., Delange A.M., McFadden G.;
RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RT telomeric region of the Shope fibroma virus genome.";
RL Virology 160:20-30(1987).
RN [2];
RP FUNCTION.
RX MEDLINE=9107415; PubMed=1850261;
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrar T., Upton C.,
RA McFadden G., Goodwin R.G.;
RT "2 open reading frame from the Shope fibroma virus encodes a soluble
RT form of the TNF receptor.";
RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE PREVENTAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M17433; -; NOT_ANNOTATED_CDS.
DR EMBL: A23727; CA01687.1; -.
DR PIR: B43692; B43692.
DR HSSP: P19438; 1TNR.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00500; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 325
FT DOMAIN 17 186
FT REPEAT 27 186
FT REPEAT 27 186
FT REPEAT 63 104
FT REPEAT 105 147
FT REPEAT 148 186
FT CARBOHYD 105 105
FT CARBOHYD 181 181
FT CARBOHYD 205 205
FT CARBOHYD 238
SQ SHOUDNCE 325 AA; 35132 MW; 81053039198A71E CnC64;

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alignment\_scores:



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296 GCAACGCTCTTCGGGGAGCGCTGAGAGGACGAGCGGCTGCGACGCC 345
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82 ysasnhlsarlgsergly.....sergluleuylsglnasngyltrpro 96
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346 ACCCAACACCGCTGCGCGCGCGCGCGCGCGCTTCTTCCGACGCGCTG 395
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
97 ThrluasprphrValCyselncysary..... 105
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
396 TTTCTGCTTGAGACGACGCTGTCCACCTGCTGCGGCGTATGCGCC 445
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
106 .....P 106
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
446 CGGGGACCC...CCGACCCGAGAACAG.....CAGTGC 474
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
106 rogllythrlnProarglnasprserlshlysluuglyValaspcys 122
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475 CAGCGCTGCGCGCGCGCGCGCGCTTCTCAGCGACGCTCCAGCTCAGAGCA 524
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123 ValProcySproProglYshlsph.....SerProglYserasnglnal 137
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
525 GTGCCAGACCCGACCGGACCTGTCAGCGCGCGCTGCGCGCTCATGTGC 574
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
137 acyslySproTrpThrlnasngylshlsuerglyLysglnllearghlsr 154
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575 CAGCGCTTCTTCCGCGCGCGCGCGCGCGCTGCGCGCTGCGCGCTGCC 624
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154 rolaaserlnasrleuaspthrValalCysgluaspargsr.....Leu 168
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
625 CTCAGGACGAGGGGTACGAGAG.....CTGAGGAGTGTGA 659
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
169 leuAlatThrleuLeu.TyrGluThrGlnargThrThrPheargProThrT 185
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
660 GCGTGGCGCTCATGAGCTTGTGGCTTTCGAGGACATCTCATCAAGAGGC 709
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
185 hvalProserThrThrValTrp...ProargThrser.Glnleuprose 200
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710 TCGCAGCGCGCTGCGCGCGCGCGCGCGCGAGCGCGCGA.....G 744
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200 rThrProThrleuValAlaProgluLysProAlaPheAlaValleLeng 217
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
745 GGCTGGGG 752
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
217 lylengly 219
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seq_name: SwissProt_39:OX40_HUMAN
seq_documentation_block:
ID OX40_HUMAN STANDARD; PRT; 277 AA.
AC P43489; O13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TRX-TRANSCRIPTIONALLY
DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).
GN TNFRSF4 OR TNXP1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94170844; Pubmed=7510240;
RA Latza U., Duerkop H., Schultiger S., Ringeling J., Eitelbach F.,
RA Hummel M., Ponatsch C., Stein H.;
RA "The human OX40 homolog: cDNA structure, expression and chromosomal
RT assignment of the ACT35 antigen.";
RL Eur. J. Immunol. 24:677-683(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=95219871; Pubmed=7704935;
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA Watson M.L., Seidlin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT "Identification of OX40 ligand and preliminary characterization of

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RT its activities on OX40 receptor.";
RL Circ. Shock 44:30-34(1994).
CC - FUNCTION: RECEPTOR FOR THE OX40L/SP34 CYTOKINE.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - SIMILARITY: CONTAINS A TA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC - DATABASE: MADE-PROT; NOTE-CD guide CD134 entry.
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".
CC -----
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CC or send an email to license@lsb.slb.ch).
CC -----
DR EMBL: X75962; CAA53576.1; -.
DR EMBL: S76792; AAB33944.1; ALT_INIT.
DR HSP: P25942; 1CDF.
DR MIM: 600315; -.
DR InterPro: IPR01368; -.
DR Pfam: PF00020; TNFR_c6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS00500; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT CHAIN 1 28 POTENTIAL.
FT DOMAIN 29 277 OX40L RECEPTOR.
FT TRANSMEM 215 214 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 236 277 POTENTIAL.
FT DOMAIN 30 169 CYTOPLASMIC (POTENTIAL).
FT REPEAT 30 65 4 X TNFR-CYS.
FT REPEAT 66 107 TNFR-CYS 1.
FT REPEAT 108 126 TNFR-CYS 2.
FT REPEAT 127 167 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 146 166 TNFR-CYS 4.
FT CARBOHYD 160 160 N-LINKED (GLCNAC... ) (POTENTIAL).
FT SPOUNCE 277 AA; 29340 MW; 49F1525941550BF CRC64;
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Quality: 230.00 Length: 313
Percent Similarity: 46.006 Percent Identity: 27.796
align_block:
US-09-006-352-1 x OX40_HUMAN ..
Align seg 1/1 to: OX40_HUMAN from: 1 to: 277
40 GGGCGAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 89
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11 GTPProcySAlaAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 27
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
90 GCGCGTCCGCGCTGTACGCGGAGTGCAGAAACACCCAGCTACCCCTGCGC 139
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
27 rglYleuHlscysVal.....GlyAspThrTyProSerA 39
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
140 GGGAGCGAGAGACGAGGAGCGCGCTGTGCTGCGCGCGCGCGCGCGCGCGC 189
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
39 snasparlg.....CysCysHlsgluCysAsrProglY 49
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190 ACCTTGTGAGGCGCGCGCGCGCGCGAGAACGCCCGCGAGCGTGTGCGCC 239
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
50 AsnolYelValserargysrserargserglinsnhrValalCysarpr 66
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
240 GTGTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 283
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
66 ocysglYProglYrPhelYAsnAspValalValserlshlyProcyLysrP 83
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
284 GCTGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 333
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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83  roCysThrTrpCysAsnLeuArgSerGly.....SerGluArgGlySerGln 97
334  GCTTGCACGCGCCACCCACACACCGCTGCTGCGCGCGCCGACCGGCTTCTT 383
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98  LeuGlyThrAlaThrGlnAspThrValCysArgCysArgAlaGly..... 112
384  GCGGACGCGCTGTTCTGCTGAGACGACGATCGTCCACTGCTGCGCG 433
      ||| |||||
113  .....ThrGlnProLeuAspSerTyrGlySerProGly.... 122
434  GCGTGAATGCCCCGCGGACCCCGACCCAGAACACGAGTGCAGCGCCG 483
123  .....ValAspCysAlaProGly 128
484  CCCCCAGGACACCTTCTGACCGACGAGTCCAGTCCAGACGAGTGCAGCC 533
      ||||| ||| ||| :|||: ||||| |||||
129  ProProGlnHisPhe.....SerProGlnAspAsnGlnAlaCysLysPyr 143
534  CCACCGCACTGACAGCGCGCTGGCGCTGGCCCTCATATGCGACGCTCTT 583
      | ||||| ||| ||| |||||
143  oTrpThrAsnCysThrLeuAlaGlyLysHisThrLeuGlnProAlaSerA 160
584  CCTGCCATGACACCGCTGTCACAGC.....TGCACGCGCTTCCCG 624
      :||| |||: |||: |||: |||: |||: |||
160  snSerSerAspAlaAlaIleCysGlnAspArgAspProProAlaThrGlnPro 176
625  CTCACGACACGAGTACACGAGCTAGAGAGTGTGAGCTGCCGTCATCGA 674
      :|||: ||| ||| ||| ||| ||| ||| |||
177  GlnGlnThrGlnGlyProProAlaArgProIleThrValGlnProThrG 193
675  CTTTGCGCTTCCAGGACATCTCCATCAGAGGCTGCAGCGGCTGCTGC 724
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193  IuAlaTrp...ProArgThrSer..... 199
725  AGGCGCTGAGGCGCGGAGGCTGGGCTCCGACACAGGCGGCGCGCG 774
200  .....GlnGlyProSerThr 204
775  GCGGCTTGCAGCTGAAGCTGCTGCGCGGCTGCACGAGCTGCGGCGG 824
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204  ArgProValGlu.....ValProGly... 211
825  GCAGAGCGGCGGCTGCTGCTGCGGCTCTGCAGCGCTGCGGCGGCGCA 874
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212  ..GlyArgAlaValAlaAlaIleLeuGlyLeuGlyValLeuGly.. 226
875  GGATGCGCGGCTGAGGCGGAGCGCTGAGCGCTGCTGCTGCTGCTGAC 924
227  .....LeuLeuGlyProLeuAlaI 233
925  TGATCTGCGCGCGCTTATTTATTTATTCATCTCTT 959
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233  IeLeuLeuAla.....LeuTyrLeuLeu 240

seq_name: SwissProt_39:VT2_MXVYL

seq_documentation_block:
ID      VT2_MXVYL      STANDARD:      PRT:      326 AA.
AC      p29825:
DT      01-APR-1993 (Rel. 25, Created)
DT      01-APR-1993 (Rel. 25, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
OS      Myxoma virus (strain Lausanne).
OC      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC      Leporipoxvirus.
OX      NCBI_TaxID=31530;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=91335768; PubMed=1651597;
RA      Upton C., Macen J.L., Schreiber M., McFadden G.;
      "Myxoma virus expresses a secreted protein with homology to the tumor
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RT      necrosis factor receptor gene family that contributes to viral
RT      virulence."
RL      Virology 184:370-382(1991).
CC      -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC      REACH CELLULAR TARGET AND THEREBY DEAPENING THE POTENTIAL
CC      ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC      -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC      -----
CC      CC THE SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
CC      BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION
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CC      MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
CC      OR SEND AN EMAIL TO LICENSE@lsb-sib.ch).
CC      -----
DR      EMBL: M95181; AAA46632.1; -.
DR      EMBL: A23729; CA01688.1; -.
DR      PIR: A40566; GQVZML.
DR      HSSP: P19438; 1TNR.
DR      InterPro: IPR001368; -.
DR      Pfam: PF00020; TNFR_c6; 2.
DR      PROSITE: PS00652; TNFR_NGFR_1; 2.
DR      PROSITE: PS50050; TNFR_NGFR_2; 2.
KW      Receptor; Glycoprotein; Repeat; Signal.
FT      SIGNAL 1 16
FT      CHAIN 17 326
FT      DOMAIN 27 186
FT      REPEAT 27 62
FT      REPEAT 63 104
FT      REPEAT 105 147
FT      REPEAT 148 186
FT      CARBOHYD 66 66
FT      CARBOHYD 181 181
FT      CARBOHYD 205 205
FT      CARBOHYD 238 238
SQ      SEQUENCE 326 AA; 35208 MW; ABBF027E947292FF CRC64;

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      Ratio: 2.072      Gaps: 6
      Percent Similarity: 53.061      Percent Identity: 30.612

alignment_block:
US-09-006-352-1 x VT2_MXVYL
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11  ValAlaCysValTyrGlyGlyGlyAlaProTyrGlyAlaAspArgGlyLys 27
101  CTGATCGCGGAGTGGCAGAAACCCACCTACCTGCGCGGAGCAGAG 150
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27  scysArgGly.....AsnAspTyrGlu 34
151  ACAGGCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 200
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35  Lys...AspGlyLeuCysCysThrSerCysProProGlySerTyrAlaSer 50
201  GCGGCGGTGCGCGCGGAGACGCGCGCGAGCGTGTGCGCGCGTGCACCGC 250
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50  ArgLeuGlyGlyProGlySerAspThrValCysSerProCysLysAsnG 67
251  GCGACTACAGCGAGTCTGGAACACTGAGAGCGCTGCCGCTACTGCAC 300
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67  IuThrPheThrAlaSerThrAsnHisAlaProAlaCysValSerCysArg 83
301  GTCCTCTGCGGCGGAGCGCTGAGAGGAGGAGGAGGCTGTCACCGCACCGCA 350
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84  GlyArgCysThrGlnHisLeuSerGlnSerGlnSerCysAspLysThrAr 100
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452 .CCCCAGCCAGAACGACGAGTCCAGCCGCGCCCGCCAGGACCTTCTC 500
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238 rProthAlaAlaProAlaAlaProAlaProAlaAlaProAlaProSer 255
501 AGCCAGCAGCTCCAGCTCAGACGAGTCCAGCCCGCCAGGACGAGCG 550
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255 rProAlaAlaProAla.....ProAlaAlaProAla... 265
551 CCCGCGCCCTGGCCCTCAATGTCAGGCTCTTCCATGACATGACCCCTG 600
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266 .....AlaAlaProProProProProPr 273
601 TGCACGAGCTGACACTGCTCCCTCAGACCGAGGTACGAGAGCTGA 650
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273 oAlaProAlaThrLeuAlaArPro.....ProGlyHisPro..... 285
651 GGAAGTGTAGAGGTGCGGCATCGACTTGTGGCTTCCAGACATCTGCA 700
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286 .....AlaGlyPro 288
701 TCAAGAGCTGACGCGCTGCTGAGCCCTCGAGCCCGGAGGGCTGC 750
||||| ||||| ||||| ||||| ||||| ||||| |||||
289 .ProThrAlaAlaProAlaAlaProProPro.....A 299
751 GGTCCGACACACAGGGCGGCGCGGCGCTTGCAGCTGAAGTGGCTG 800
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299 lAlaAlaAlaGlnAsnGlySerAlaGlyAlaAlaProAlaProAlaPro 315
801 GCGGCTGACGAGCTCGTGGGCGGCGAGCGGCGCTGCTGTGGTGGC 850
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316 AlAlaAlaGlyProAlaGlyAlaSerGlyInProGlyProGlyAlaAl 332
851 TGTGTCAGCGCTGCGGCTGCGAGTGCAGCGCGGCTGAGACGAGCTC 900
||||| ||||| ||||| ||||| ||||| ||||| |||||
332 aAlaAlaAlaProAlaProGlyAlaGlyAlaGlySerProGlyAlaV 349
901 CGTGAGCGCTTCTCTCTGTCGACTGATCTGCGCCCTCT 941
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349 aGlnAlaAlaProAlaAlaGlnThrLeuAlaAlaSer 362

seq_name: SwissProt_39:CD40_HUMAN

seq_documentation_block:
ID CD40_HUMAN STANDARD; PRT; 277 AA.
AC P25942;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40)
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89356608; PubMed=2475341;
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RT factor receptor and induced by cytokines in carcinomas.";
RL EMBO J. 8:1403-1410(1989).
RN [2]
RN 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Bajorath J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40.";
RL Proteins 27:59-70(1997).
RN [3]
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX MEDLINE=98266353; PubMed=9605317;
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
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RA Zheng Z., Naismith J.H., Thomas D.;
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -1- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm"
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb.slb.ch).
CC
DR EMBL: X60592; CAA43045.1; -
DR PIR: S04460; S04460.
DR PDB: 1CDE; 01-APR-97.
DR MM: 109535; -
DR InterPro: IPR001368; -
DR Pfam: PF00020; TNFR_c6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS00505; TNFR_NGFR_2; 4.
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1..19 POTENTIAL.
FT CHAIN 20..277 CD40L RECEPTOR.
FT DOMAIN 20..193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194..215 POTENTIAL.
FT DOMAIN 216..277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25..187 4 x TNFR-CYS.
FT REPEAT 25..60 TNFR-CYS 1.
FT REPEAT 61..103 TNFR-CYS 2.
FT REPEAT 104..144 TNFR-CYS 3.
FT REPEAT 145..187 TNFR-CYS 4.
FT DISULFID 26..37
FT DISULFID 38..51
FT DISULFID 41..59
FT DISULFID 62..77
FT DISULFID 83..103
FT DISULFID 105..119
FT DISULFID 111..116
FT DISULFID 125..143
FT CARBOHYD 153..153
FT CARBOHYD 180..180
FT SEQUENCE 277 AA; 30619 MW; BC8776EC2CA5680 CRC64;
N-LINKED (GLCNAC... ) (POTENTIAL).
N-LINKED (GLCNAC... ) (POTENTIAL).

alignment_scores:
Quality: 211.00 Length: 151
Ratio: 2.512 Gaps: 3
Percent Similarity: 55.629 Percent Identity: 30.464

alignment_block:
US-09-006-352-1 x CD40_HUMAN ..

Align seq 1/1 to: CD40_HUMAN from: 1 to: 277

169 TGGCGCCAGTGCCTCCCGCCAGGACCTGTTGTGACGCGCGCTGCGCGAGGA 218
||||| ||| ||||| ||||| ||||| ||||| |||||
38 CysSerLeuGlyGlnProGlyGlnLeuValSerAspCysThrGluPh 54
219 CAGCCCGCAGAGGTGTGGCCGTGTCCACGCGCCGACTACAGCAGTTCT 268
||| ||| ||| ||||| ||||| ||||| |||||
54 eThrGluThrGlyLeuProCysGlyGluSerGluPhLeuAspThrT 71
269 GGAAGTGTAGAGGTGCGGCATCGACTTGTGGCTTCCAGACATCTGCG 309
||||| ||||| ||||| ||||| ||||| ||||| |||||
71 rPasnArGgluThrHisCysHisGlnHisLysTyrcysAspProAsnLeu 87
```











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OM of: US-09-006-352-1 to: SPTRMBL\_16.\* out\_format : pfs

Date: Oct 31, 2001 12:33 PM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

#### Command line parameters:

```
-MODEL=frame+12p_model -DEV=x1h  
-O=/cgn2.1/USPTO_spool/US09006352/runat_30102001.104618.3376/app-query.fasta_1.1150  
-DB=SPTRMBL_16 -OPMT=fastan -SUFFIX=rspt -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000  
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-EGAPOP=6.000 -EGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELCP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blotsum62  
-TRANS=ham40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pcr  
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NORM=ext -MINLEN=0 -MAXLEN=200000000  
-USER=US09006352 -CGN1_1_147 -NCPU=6 -ICPU=3 -LONGLOG  
-DEV=US09006352 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1
```

#### Search information block:

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Query: US-09-006-352-1  
Query length: 1077  
Database: SPTRMBL_16.*  
Database sequences: 425026  
Database length: 13305027  
Search time (sec): 68.61000
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Sequence	Strd Orig	ZScore	Escore	Len	Documentation
SP_human:095407	1634.00	1506.18	2.0e-98	300	095407 homo sapiens (human). de
SP_human:099874	541.00	626.64	9.6e-28	1161	099874 homo sapiens (human). de
SP_human:094771	533.00	616.25	3.0e-27	1400	094771 homo sapiens (human). de
SP_human:094802	533.00	630.26	7.0e-27	100	094802 homo sapiens (human). de
SP_human:090300	444.00	516.25	2.5e-21	401	090300 homo sapiens (human). os
SP_human:090494	440.50	519.25	4.2e-21	372	090494 homo sapiens (human). os
SP_rident:008727	425.50	498.36	3.9e-20	401	008727 rattus norvegicus (rat). os
SP_rident:008712	424.50	497.20	4.5e-20	401	008712 mus musculus (mouse). os
SP_vertebrate:09PUS0	395.00	464.50	4.0e-18	302	09PUS0 salvelinus fontinalis (t
SP_rident:063327	342.50	401.01	9.0e-15	439	063327 mus musculus (mouse). tu
SP_human:016614	340.50	398.94	1.2e-14	459	016614 homo sapiens (human). tu
SP_rident:088734	336.00	393.17	2.3e-14	482	088734 mus musculus (mouse). p8
SP_rident:098PUS5	292.00	340.21	1.5e-11	655	098PUS5 mus musculus (mouse). de
SP_human:075509	289.00	336.71	2.4e-11	655	075509 homo sapiens (human). tu
SP_virus:057277	282.50	332.79	7.5e-11	348	057277 monkeypox virus. tumor n
SP_virus:057103	280.50	330.46	1.0e-10	348	057103 monkeypox virus. tumor n
SP_virus:057108	276.00	330.46	1.0e-10	348	057108 monkeypox virus. tumor n
SP_virus:057108	276.00	325.21	2.0e-10	349	057108 monkeypox virus. tumor n
SP_virus:057100	274.00	322.88	2.7e-10	349	057291 monkeypox virus. tumor n
SP_virus:057291	274.00	322.88	2.7e-10	349	057101 monkeypox virus. tumor n
SP_virus:057102	274.00	322.88	2.7e-10	349	057102 monkeypox virus. tumor n
SP_virus:057099	263.00	321.72	3.1e-10	349	057099 monkeypox virus. tumor n
SP_virus:057116	263.00	312.39	1.0e-09	350	057116 cowpox virus (cpv). tunc
SP_virus:085308	264.50	311.73	1.1e-09	355	085308 cowpox virus (cpv). sect
SP_virus:085308	264.50	309.50	1.5e-09	349	057110 variola virus. tumor nec
SP_virus:057110	262.50	309.50	1.5e-09	349	057111 variola virus. tumor nec
SP_virus:089118	262.50	309.50	1.5e-09	349	089118 variola virus. somalia-1
SP_virus:089098	262.50	309.50	1.5e-09	349	089098 variola virus. and vari
SP_virus:057112	262.00	308.94	1.6e-09	348	057112 variola virus. tumor nec
SP_virus:085407	262.00	308.94	1.6e-09	348	085407 variola virus. homolog c
SP_virus:057284	261.50	308.34	1.7e-09	349	057284 cowpox virus (cpv). tunc
SP_virus:057098	261.50	308.34	1.7e-09	349	057098 cowpox virus (cpv). tunc
SP_virus:057305	258.50	306.01	2.3e-09	349	057305 cowpox virus (cpv). tunc
SP_virus:057118	259.50	305.83	2.3e-09	360	057118 cowpox virus (cpv). tunc
SP_virus:057117	258.50	304.81	2.7e-09	351	057117 cowpox virus (cpv). tunc
SP_virus:073559	258.50	304.81	2.7e-09	351	073559 cowpox virus (cpv). h4c
SP_virus:057120	257.50	304.07	3.2e-09	326	057120 cowpox virus (cpv). tunc
SP_virus:057097	257.50	303.68	3.1e-09	349	057097 cowpox virus (cpv). tunc
SP_invertebrate:09GUW7	256.50	294.08	2.5e-09	1514	09GUW7 leishmania major. 184
SP_virus:057122	254.50	300.58	5.0e-09	326	057122 cowpox virus (cpv). tunc

SP_virus:057109	254.50	300.19	4.9e-09	349	057109 variola virus. tumor
SP_virus:057115	253.50	299.06	5.7e-09	347	057115 cowpox virus (cpv). t
SP_virus:057119	251.50	296.73	7.6e-09	347	057119 cowpox virus (cpv). t
SP_virus:057121	250.50	295.51	8.8e-09	351	057121 cowpox virus (cpv). t
SP_mammal:09XSZ8	249.00	295.00	1.2e-08	283	09XSZ8 cercopithecus aethiop

seq\_name: SP\_human:095407

#### seq\_documentation\_block:

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ID 095407 PRELIMINARY; PRT; 300 AA.  
AC 095407;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1).  
GN DCR3 OR TR6 OR TNFRSF6B.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99087326; PubMed=9872321;  
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,  
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,  
RA Goddard P.J., Wood W.I., Gunney A.L., Hillan K.J., Cohen R.L.,  
RA Goddard A.D., Botstein D., Ashkenazi A.;  
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and  
RT colon cancer.";  
RL Nature 396:699-703(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BLOOD;  
RX MEDLINE=99253915; PubMed=10318773;  
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;  
RT "A newly identified member of tumor necrosis factor receptor  
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";  
RL J. Biol. Chem. 274:13733-13736(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PANCREAS;  
RX MEDLINE=20122600; PubMed=10655513;  
RA Pat C., Connolly B., Metzker M.B., Hilliard C.A., Liu X., Sandig V.,  
RA Soderman A.G., Gallaway S.M., Liu Q., Austin C.P., Caskey C.T.;  
RT "Overexpression of M68/DCR3 in human gastrointestinal tract tumors  
RT independent of gene amplification and its location in a four-gene  
RT cluster.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Matthews L.;  
RL Submitted (NCV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF104419; AAD03056.1; -  
DR EMBL: AF134240; AAD29688.1; -  
DR EMBL: AF217796; AAF35244.1; -  
DR EMBL: AF217793; AAF33685.1; -  
DR EMBL: AF217794; AAF33686.1; -  
DR EMBL: AF121845; CAC03668.1; -  
DR HSSP: P25942; ICDF.  
DR InterPro: IPR000561; -  
DR InterPro: IPR001368; -  
DR Pfam: PF00020; TNFR_c6; 4.  
DR ProDom: PD000771; -; 1.  
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.  
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.  
DR PROSITE: PS00502; TNFR_NGFR_2; 2.  
KW Receptor.  
SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;
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#### alignment\_scores:

Quality: 1634.00 Length: 300  
Ratio: 5.447 Gaps: 0



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seq_name: sp_human:Q9NZ71
seq_documentation_block:
ID Q9NZ71 PRELIMINARY; PRT; 1400 AA.
AC Q9NZ71;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE HELICASE-LIKE PROTEIN NHL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20122600; PubMed=10655513;
RA Bal C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M66/DCR3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster."
RT Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
DR EMBL; AF217796; AAF35243.1;
SQ SEQUENCE 1400 AA; 152373 MW; F3F2BB93D48ED3D9 CRC64;

alignment_scores:
Quality: 533.00 Length: 104
Ratio: 5.330 Gaps: 0
Percent Similarity: 96.154 Percent Identity: 96.154

alignment_block:
US-09-006-352-1 x Q9NZ71 ..
Align seg 1/1 to: Q9NZ71 from: 1 to: 1400

6 CCGTGTCCACCAAGACGACGAGCGGCTGGAGGGGCCAGCCCTGTGCG 55
|||||
1397 ProtiupProhiIslYsAspHIsIglYlAglYlAalArgProvalAI 1313
56 TGCTGTGCTGTGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGTA 105
|||||
1313 AAlValPrOolYalIglYlAalAalAalAalAalAalAalAalAalAal 1330
106 CGCGAGTGGCAGAAACACCCACCTACCCCTGCGGGGAGCAGAGACAGG 155
|||||
1330 hrArgSerGIYArgAsnThrIstLeuProleuAlaIglYArgAspArg 1346
156 GGACGGCTGTGTGCGCCGACGCTGCGCCCGCAGACCTTTGTGACGGCGC 205
|||||
1347 GYlAlAalAalIglYalAalAalAalAalAalAalAalAalAalAal 1363
206 CGTGGCGCGGAGACAGCCGACGCTGTGCGCTGCTGCTGCTGCTGCTGCT 255
|||||
1363 aValPrOolrGlnPrOhiIslAspValTTPProvalSerThrAlaProL 1380
256 TACACGAGTGTGGAACCTACCTGAGCGCTGCGCTGCTGCTGCTGCTGCT 305
|||||
1380 euHIsAlaValleuGlueuProGIYalAalAalAalAalAalAalAal 1396
306 CTGCGGGGAGCG 317
|||||
1397 LeuArgGIYAla 1400

seq_name: sp_human:Q9HA02
seq_documentation_block:
ID Q9HA02 PRELIMINARY; PRT; 100 AA.
AC Q9HA02;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE D583P15.9 (K1A1088) (FRAGMENT).

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```

GN BK3184A7.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121845; CAC16546.1;
FT NON TER 1 1
SQ SEQUENCE 100 AA; 10169 MW; 44BA216B2A028007 CRC64;

alignment_scores:
Quality: 532.00 Length: 100
Ratio: 5.374 Gaps: 0
Percent Similarity: 99.000 Percent Identity: 99.000

alignment_block:
US-09-006-352-1 x Q9HA02 ..
Align seg 1/1 to: Q9HA02 from: 1 to: 100

18 AAGACCAATGAGGCGCTGAGAGGGCCAGGCCCTGCTGCTGCTGCTG 67
|||||
1 LysAspHIsIglYlAalAalAalAalAalAalAalAalAalAalAal 17
68 TGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 117
|||||
17 YalGIYAlAalAalAalAalAalAalAalAalAalAalAalAalAal 34
118 GAACACCCACCTACCCCTGCGGGGAGCAGAGAGGAGGAGCGCTGCT 167
|||||
34 rGAsnThrIstLeuProleuAlaIglYArgAspArgYlAalAalAal 50
168 GTGGCGCCAGTGGCGCCCGCAGCACCCTTTGTGCAGCGCGCTGCCGCGAG 217
|||||
51 ValArgProvalPrOolrGlnPrOhiIslAalAalAalAalAalAalAal 67
218 ACAGCGCCGAGAGCTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 267
|||||
67 gLPrOhiIslAspValTTPProvalSerThrAlaProleuHIsAlaVal 84
268 TGAACCTACTGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 317
|||||
84 euGlueuProArgAlaIleuProleuGlueuAlArgProleuArgGIYAla 100

seq_name: sp_human:000300
seq_documentation_block:
ID 000300 PRELIMINARY; PRT; 401 AA.
AC 000300; 060236;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOCYTES INHIBITORY FACTOR)
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=KIDNEY;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RA He Z.-Y., Yang G.-Z., Zhang W.-J., Mu X.-F.;  
 RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";  
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).  
 DR EMBL; AF134187; AAF20168.1;  
 DR HSSP; P25942; 1CDF.  
 DR InterPro: IPR000488;  
 DR InterPro: IPR001368;  
 DR Pfam: PF00020; TNFR\_c6; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE: PS00650; TNFR\_NGFR\_2; 2.  
 DR SMART: SM00005; DEATH; 1.  
 FT NON\_TER 1  
 SO SEQUENCE 372 AA: 42758 MW: F02527A5CD01CCD3 CRC64;

alignment\_scores:  
 Quality: 440.50 Length: 187  
 Ratio: 3.469 Gaps: 2  
 Percent Similarity: 67.914 Percent Identity: 41.176

alignment\_block:  
 US-09-006-352-1 x Q9UHP4 ..

Align seg 1/1 to: Q9UHP4 from: 1 to: 372

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124 CCCACCTACCCCTGGCGGAGACAGACAGGCGCGTGTGCGC 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
5  ProlystylLeuHisTyrAspGluThrSerHisGlnLeuLeuCyAs 21
174 CCAGGCGCGCGCGACCTTTGTGACGCGCGCGCGCGCGAGACACC 223
    : : : : : : : : : : : : : : : : : : : : : : : :
21  pLysCysProPheGlyTyrLeuTyrGlnHisCysThrAlaTyrPL 38
224 CCACGACCTGTGGCGCGCTGTCCACGCGCGCGACGACGCTTGTGAC 273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
38  ystHValGlyAlaProCysProAspHisTyrTyrThrAspSerThr 54
274 TACCTGGAGCGCTGCGCTACTGACAGCTCTGTGGGAGCGGTGAGCA 323
    : : : : : : : : : : : : : : : : : : : : : : : :
55  ThrSerAspGluCysLeuTyrCysSerProValCysLysGlnLeuGln 71
324 GGAGGACGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCA 373
    : : : : : : : : : : : : : : : : : : : : : : : :
71  fValLysGlnGluCysAsnArgThrHisAsnArgValCysGluCysLys 88
374 CCGGCTTCTTCCGCGACGCTGTTTCTGTGAGACGACGATCGTGTCCA 423
    ||| : : : : : ||| ||| ||| ||| ||| ||| ||| |||
88  lGluArgTyrLeuGlnIleGluThrCysLeuLysHisArgSerCysPro 104
424 CTTGTGCGCGCGTGATGCGCGCGCGCGCGCGCGCGCGCGCA 473
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
105  ProGlyPheGlyValAlaGlnAlaGlyThrProGluArgAsnThrVal 121
474 CCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 523
    : : : : : : : : : : : : : : : : : : : : : : : :
121  sLysArgCysProAspGlyPhePheSerAsnGluThrSerSerLysAla 138
524 AGTCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 573
    ||| : : : : : ||| ||| ||| ||| ||| ||| ||| |||
138  rocYsArgLysHisThrAsnCysSerValPheGlyLeuLeuLeuThrIn 154
574 CCAGGCTTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 623
    ||| : : : : : ||| ||| ||| ||| ||| ||| ||| |||
155  LysGlyAsnAlaThrHisAspAsnLeu.....CysSerGlyAsnSe 168
624 CCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
168  rGluSerThrGlnLysCysGlyIleAspValThrLeuCysGlnGluAla 185
  
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seq_name: sp_rodent:008727
seq_documentation_block:
ID 008727 PRELIMINARY; PRT: 401 AA.
AC 008727;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OSTEOCLASTOGENESIS INHIBITORY FACTOR (OICIF).
GN TNFRSF1B OR OPG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luetthy R., Nguyen H.Q., Wooden S., Bennett L., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Dery P., Lee R.,
RA Suggs S., Boyle W.J.,
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density."
RL Cell 89:309-319(1997).
CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: U94330; AAB5707.1; -.
DR HSSP; P25942; 1CDF.
DR InterPro: IPR000488; -.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; -.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00650; TNFR_NGFR_2; 2.
DR SMART; SM00005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT DOMAIN 23 201 4 X TNFR-CYS.
FT REPEAT 23 63 TNFR-CYS 1.
FT REPEAT 64 106 TNFR-CYS 2.
FT REPEAT 107 143 TNFR-CYS 3.
FT REPEAT 144 201 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 401 AA: 46192 MW: FEC6A31F1D4E573A CRC64;
  
```

Mon Nov 5 08:22:35 2001

us-09-006-352-1.rsp1

Page 6

alignment\_scores:                   Quality: 425.50                   Length: 205  
                                     Ratio: 3.199                   Gaps: 2  
Percent Similarity: 64.878           Percent Identity: 39.512

alignment\_block:  
US-09-006-352-1 x 008727                   ..

Align seg 1/1 to: 008727 from: 1 to: 401

```
124 CCACCTACCTGCGGCGGACGACGAGGAGGAGCGGCTGGTGGCC 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
26 ProllytYrLeuHISTyrAspProGlnHrHsAsnAlaGAGAG 42
    : : : : : : : : : : : : : : : : : : : : : : : :
174 CCAAGTCCCCCGACCTTTGTGACGCGCGCGCGCGGACAGACC 223
    : : : : : : : : : : : : : : : : : : : : : : : :
42 pLysCysAlaProGlyThrYrLeuYsGlnHsCysThrValAGAG 59
    : : : : : : : : : : : : : : : : : : : : : : : :
224 CCAAGCTGTGGCGCGCGGTGCGGCGGACGACGAGATTGTGAGC 273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
59 ThrLeuYsValProCysProAspYrSerYrThrAspSerTrpHis 75
    : : : : : : : : : : : : : : : : : : : : : : : :
274 TACCTGAGAGCGCTGCGCTACTGACAGCTCTGCGGAGAGCTGAGA 323
    : : : : : : : : : : : : : : : : : : : : : : : :
76 ThrSerAspGluCysValYrCysSerProValCysLysGlnLeuGln 92
    : : : : : : : : : : : : : : : : : : : : : : : :
324 GAGAGCGCGGCTTGCACAGCCACGACGACGCTGCGCGCGCGCA 373
    : : : : : : : : : : : : : : : : : : : : : : : :
92 ValYsGlnGluCysAsnAlaGlnHrHsAsnAlaGValCysGluCys 109
    : : : : : : : : : : : : : : : : : : : : : : : :
374 CCGGCTTCTTCCGCGACCGCTGTTCTGTGAGAGCAGCATGCTGCA 423
    ||| : : : : : : : : : : : : : : : : : : : : : :
109 IndYrGlyYrLeuGlnLeuGlnHrHsCysLeuYsHsAspSerCys 125
    : : : : : : : : : : : : : : : : : : : : : : : :
424 CCGTGGCGCGGCTGATGCGCGCGGCGGCGGACGAGAGGAG 473
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
126 ProGlyLeuGlyValLeuGlnAlaGlyYrHrProGlnHrAsnAla 142
    : : : : : : : : : : : : : : : : : : : : : : : :
474 CCAAGCGTGGCGCGGCTTGTGACGAGCAGCTGACGCTGAGAGC 523
    : : : : : : : : : : : : : : : : : : : : : : : :
142 sLysAlaGlySerProAspGlyHrHsAspSerGlyGlnHrSerLeu 159
    : : : : : : : : : : : : : : : : : : : : : : : :
524 AGCGGACGCGCGGCGGACGAGCTGCGCGCGGCGGCGGCGGATG 573
    : : : : : : : : : : : : : : : : : : : : : : : :
159 rOcYsArGlyHsHsThrAsnGlySerLeuGlnLeuLeuLeuGln 175
    : : : : : : : : : : : : : : : : : : : : : : : :
574 CCAAGGCTTCTGCTCCATGACAGCCCTGTGACAGCTGAGCTGCC 623
    : : : : : : : : : : : : : : : : : : : : : : : :
176 LysGlyAsnAlaThrHsAspAsnVal.....CysSerLeuYsAsn 189
    : : : : : : : : : : : : : : : : : : : : : : : :
624 CCTGACGACGCGGCTTACGAGAGCTGAGAG.....TTGAGCGTGGC 667
    : : : : : : : : : : : : : : : : : : : : : : : :
189 gGluAlaThrGlnAsnGlyLeuAspValThrLeuYsGlnGluAla 206
    : : : : : : : : : : : : : : : : : : : : : : : :
668 TCATGCACTTGTGCTTCCAGAGCATTCATCAAGAGCTGACGCG 717
    : : : : : : : : : : : : : : : : : : : : : : : :
206 hePheHrPheAlaValProThrYsIleLeuProAsnThrLeuSer 222
    : : : : : : : : : : : : : : : : : : : : : : : :
718 CTGCTGACGCGGCTC 732
    : : : : : : : : : : : : : : : : : : : : : : : :
223 LeuValAspSerLeu 227
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seq\_name: sp\_froden1:008712

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seq_documentation_block:
ID 008712 PRELIMINARY: PRT: 401 AA.
AC 008712: 070202;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
(OcIF).
```

```
GN TNFRSF1B OR OPB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
PN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAID/C; TISSUE=KIDNEY;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.U., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luehly R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Ola, AND NIH SWISS;
RX MEDLINE=98382527; PubMed=9714833;
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA Higashio K.;
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OcIF)
RT gene and its expression in embryogenesis.";
RL Gene 215:339-343(1998).
RC [1]
-1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
CC PLACENTA. NOT DETECTED IN THE EMBRYO. HIGH LEVELS ARE DETECTED AT
CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
CC DAY 7 AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
CC 15 TO DAY 17.
CC CC
DR -1- SIMILARITY: CONTAINS A LA-NGF/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: AB013898; BAA28269.1; .
DR EMBL: AB013903; BAA33388.1; .
DR EMBL: AB013899; BAA33388.1; JOINED.
DR EMBL: AB013900; BAA33388.1; JOINED.
DR EMBL: AB013901; BAA33388.1; JOINED.
DR EMBL: AB013902; BAA33388.1; JOINED.
DR HSSP: P25942; ICDF.
DR MGI: MGI:109587; Tnfrsf1b.
DR InterPro: IPR00488; .
DR InterPro: IPR001368; .
DR Pfam: PF00020; TNFR_c6; 3.
DR ProDom: PD000771; -; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR SMART: SM00005; DEATH; 1.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT DOMAIN 23 201 4 X TNFR-CYS.
FT REPEAT 23 63 TNFR-CYS 1.
FT REPEAT 64 106 TNFR-CYS 2.
FT REPEAT 107 143 TNFR-CYS 3.
FT REPEAT 144 201 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFD 41 54 BY SIMILARITY.
FT DISULFD 44 62 BY SIMILARITY.
FT DISULFD 65 80 BY SIMILARITY.
FT DISULFD 83 97 BY SIMILARITY.
FT DISULFD 87 105 BY SIMILARITY.
FT DISULFD 118 142 BY SIMILARITY.
```

```

-206 hephaargpnehiavaIProThruylsillelleProasntRpreuSerVal 222
      718 GTCGTGACAGGCCCTC 732
          |||:|||||
          |||:|||||
223 LeuValaspsrleu 227
      718 GTCGTGACAGGCCCTC 732
          |||:|||||
          |||:|||||

seq_name: sp.vertibrate:Q9PUS0

seq_documentation_block:
ID      Q9PUS0      PRELIMINARY;      PRT:      302 AA.
AC      Q9PUS0
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-MAY-2001 (TREMBLrel. 16, Last annotation update)
DE      DECOY RECEPTOR.
OS      Salvelinus fontinalis (Brook trout) (Brook char).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC      Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX      NCBI_TaxID=8038;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Bode J., Goetz F.W.;
RT      "A tumor necrosis factor receptor homolog is up-regulated in the brook
RT      trout (Salvelinus fontinalis) ovary at the completion of ovulation.";
RL      Biol. Reprod. 0:0-0(1999).
DR      EMBL; AF156738; AAD56428.1; -.
DR      HSSP; P13438; 1EXT.
DR      InterPro; IPR000561; -.
DR      InterPro; IPR001368; -.
DR      Pfam; PF00020; TNFR_c6; 4.
DR      PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR      PROSITE; PS00652; TNFR_NCFR_1; UNKNOWN_1.
DR      PROSITE; PS50050; TNFR_NCFR_2; 1.
DR      SMART; SM00208; TNFR; 1.
DR      Receptor.
SQ      SEQUENCE      302 AA: 34037 MW; E44C73477F05C3DF CRC64;

alignment_scores:
      Quality: 395.00      Length: 239
      Ratio: 2.669      Gaps: 7
Percent Similarity: 61.925      Percent Identity: 34.310

alignment_block:
US-09-006-352-1 x Q9PUS0  ..

Align seg 1/1 to: Q9PUS0 from: 1 to: 302

127 ACCTACCCCTGGCGGACGCGACAGAGAGGGAGCGCGCTGTGGCGCCCA 176
      |||:|||||
      |||:|||||
22 TrhrpelysasnapasparatgTyrSerleYleuSerlleValalysaspar 38
      |||:|||||
      |||:|||||
177 GTGCCCCCGACGACCTTTGTGTGACGCGCGGTGGCCGCGAGACGCCCA 226
      |||:|||||
      |||:|||||
38 gcystrprohroglYhrThruYleuATgAlarProCysSerAlaMetArgLys 55
      |||:|||||
      |||:|||||
227 GCACGTGTGGCCCGGTGTGCACCGCGCCACAGACGATTTGTGGAATAC 276
      |||:|||||
      |||:|||||
55 eArspcGcyAlaGlucYsProasmnGlYalATgYrThrgluPhetrAsnHnls 71
      |||:|||||
      |||:|||||
277 GTGAGCGCGCTGTGCGCTACTGCAACGTCGTGCGGGGAGCGTAGAGGA 326
      |||:|||||
      |||:|||||
72 lleSerlyscYsleuATgCysSer..MetCysAlaLduasmnGlValVal 87
      |||:|||||
      |||:|||||
327 GGCACGAGCGCTTGCCACGCGCACACGACGACGTCGCTGCGCGACGCG 376
      |||:|||||
      |||:|||||
87 lLysInglucYsSerProSerAsnAnscYsGlucYsGlucYsGluc 104
      |||:|||||
      |||:|||||
377 GCTTTTGTGGCGCAGCGTGGTTTC.....TGCTTGGACGACGATCGTC 420
      |||:|||||
      |||:|||||
104 lYTTTgYrPheAsnlyscYsleuATgAlaLysCyslleYsHnlslyscYs 120
      |||:|||||
      |||:|||||

```



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seq_documentation_block:
ID   Q16042; PRELIMINARY; PRT; 439 AA.
AC   Q16042;
DT   01-NOV-1996 (TREMBLrel. 01, Created)
DT   01-JAN-1999 (TREMBLrel. 09, Last sequence update)
DT   01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91370690; PubMed=1966549;
RA   Dember Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
RA   Brochhaus M., Lesslauer W.;
RT   "Two human TNF receptors have similar extracellular, but distinct
RT   intracellular, domain sequences.";
RL   Cytokine 2:231-237(1990).
DR   EMBL; S63368; AAB19824.1; -.
DR   HSSP; P25942; ICDF.
DR   InterPro; IPR001368; -.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000711; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS00500; TNFR_NGFR_2; 3.
DR   SMART; SM00208; TNFR; 2.
SQ   SEQUENCE 439 AA; 46090 MW; FEBCB329CC67FF6 CRC64;

```

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alignment_scores:
Quality: 340.50      Length: 300
Ratio: 2.115         Gaps: 11
Percent Similarity: 53.667      Percent Identity: 29.667

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alignment_block:
US-09-006-352-1 x Q16042 ..

```

```

Align seg 1/1 to: Q16042 from: 1 to: 439

```

```

112 GTGGCAGAAACCCACCTACCCCTGGCGGAGCCAGACAGGAGGAG.. 159
    ||||| ||||| ||| ||| |||
5 ValAlaIheThrProTyrAlaPro.....GluProGlySerThr 17
160 .....CGCGTGGTGGCGCC 175
17 rCyAlaIheArgIleuTyrTyrAspGlnThrAlaGlnMetCysSerL 34
    :||| ||||| :||| ||| :|||
176 AGTGCACCCCGAGGACCTTTGTGCGAGCGCGTCCCGCCGAGACGCC 225
    :||| ||||| :||| ||| :|||
34 yscysSerProGlyGlnHisAlaIysValPheCysThrLysThrSerAsp 50
    ||||| ||||| ||||| ||||| |||||
226 ACAGCAGTGGCCCGTGTCCACCGCCGACCTACACGCAAGTTCTGAC 275
    ||||| ||||| ||||| ||||| |||||
51 ThrValCysAspSerCysGluAspSerThrTyrThrGlnLeuTrpAsp 67
    ||||| ||||| ||||| ||||| |||||
276 CCTGAGAGCGCGCGCTACTGCAACGTCCTCTGCGGAGGCGTGGAGG 325
    :||| ||||| ||||| ||||| |||||
67 pValIProGlnCysLeuSerCysGlySerArgCysSerSeraspGlnVal 84
    ||||| ||||| ||||| ||||| |||||
326 AGGACGAGGCTTGGCCAGCCACCAACCAACCGTCCGCGCGCCGAC 375
    ||||| ||||| ||||| ||||| |||||
84 LuthrGlnAlaIysThrArgGlnGlnAsnArgIleCysThrCysArgPro 100
    ||||| ||||| ||||| ||||| |||||
376 GGCTTTTCGGCGACGCTGTT.....TTCTGCTTGA 407
    ||||| ||||| ||||| ||||| |||||
101 GlyTyrTyrCysAlaLeuSerLysGlnGlnLysArgLeuCysAlaPr 117
    ||||| ||||| ||||| ||||| |||||
408 GCACGACATCGTGTCCACCTGTGCGGCGGATGCGCGGAGCCGCCA 457
    ||||| ||||| ||||| ||||| |||||
117 oLeuArgLysCysArgProGlyPheGlyValAlaArgProGlyThrGlu 134
    ||||| ||||| ||||| ||||| |||||
458 GCCAAGAACACGACGATGCCAGCGCGTCCCGCCGAGCACCCTTCTCA 507

```

```

seq_documentation_block:
ID   088734; PRELIMINARY; PRT; 482 AA.
AC   088734;
DT   01-NOV-1998 (TREMBLrel. 08, Created)
DT   01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT   01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE   P80 TNF-ALPHA RECEPTOR.
DE   TNFR2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT   "The Mouse Tumor Necrosis Factor Receptor Gene: Genomic Structure and
RT   Characterization of the two Transcripts.";
RL   Genomics 0:0-0(0).
DR   EMBL; Y14619; CAA74969.1; -.
DR   EMBL; Y14620; CAA74969.1; JOINED.
DR   EMBL; Y14621; CAA74969.1; JOINED.
DR   EMBL; Y14622; CAA74969.1; JOINED.
DR   EMBL; Y14623; CAA74969.1; JOINED.
DR   EMBL; Y14679; CAA74969.1; JOINED.
DR   HSSP; P19438; INCF.
DR   InterPro; IPR001368; -.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS00500; TNFR_NGFR_2; 3.
DR   SMART; SM00208; TNFR; 1.
SQ   SEQUENCE 482 AA; 51106 MW; F6C15046B48F83C CRC64;

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alignment\_scores:                      Length:                      245  
 Quality:                      336.00                      Gaps:                      11  
 Ratio:                      2.366  
 Percent Similarity:                      57.959                      Percent Identity:                      33.469

Alignment\_block:  
 US-09-006-352-1 x 088734 ..

Align seg 1/1 to: 088734 from: 1 to: 482

```

160 CGGCTGTGTGCGCCAGTGCCTGCGGACGACCTTTGTGACGCGCGTGTG 209
    ::::: |||||:::|||||:::|||||:::|||||:::|||||:::
52 GlnMetCysGlyAlaLysCysProProGlyGlnTyrValLysHisPheCys 68
210 CCGCGCA.....GACAGCGCCGACGCTGTGCGG 238
    ||:::|||||:::|||||:::|||||:::|||||:::
68 sAsnLysThrSerAspThrValCysAlaAspSerAspThrValCysAla 85
239 CGTGTCCACCGCGCCAGTGCCTGCGGACGACCTTTGTGACGCGCGTGTG 288
    ||| ||||| ||||| ||||| ||||| ||||| |||||
85 sPcysGlnLysSerMetLysThrGlnValItrPasnGlnPheAlaGlyTrpCys 101
289 CGCTACTGACAGCTCTGCGGCGGACGCTGAGAGGACGACGCGCTGTG 338
    ||:::|||||:::|||||:::|||||:::|||||:::
102 LeuSerCysSerSerSerCysSerThrAspGlnValGlnThrArgAlaCys 118
339 CCAAGCGCCACGACACCTGCGCGCGCGCGCGCGCGCGCGCTGTG... 384
    ||:::|||||:::|||||:::|||||:::|||||:::
118 sThrLysGlnGlnAsnArgValCysAlaCysGlnAlaGlyArgTyrCysA 135
385 .....CGGACGCTGTGCTTC.....TGCTTGACGACGCGCATCG 417
    ||:::|||||:::|||||:::|||||:::|||||:::
135 LalaLysThrHisSerLysSerCysArgLncCysMetArgLeuSerLys 151
418 TGTCACAGTGTGCGGCGGATGATGCGCGGACCGCGGACCGCGGACGAC 467
    ||| ||||| ||||| ::::: ||||| ::::: |||||
152 CysGlnLysProGlyPheGlyValAlaSerSerArgAlaProAsnGlyAsnVa 168
468 GCAATGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTG 517
    ::::: ||||| ||| ||||| ||||| ||||| |||||
168 LLeuCysLysAlaCysAlaProGlyThrPheSerAspThrThrSerSerT 185
518 CAGAGCAGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 567
    ::::: ||||| ||||| ||||| ||||| |||||
185 hTrsPvalCysArgProHisArgLecysSerLleLeuAla..... 198
568 AATGTCAGAGCTTCTCCATGACACCGCTGTGACGACGCGCGCGCTGTG 617
    ::::: ||||| ||||| ||||| ||||| |||||
199 ...LleProGlyAsnAlaSerThrAspAlaValCys..... 209
618 CTTCGCCCTCAGCAGGATACGAGGAGCTGAGAGTGAAGTGAAGCGCGG 667
210 .....AlaPro.GluSerProThrLleuSerAlaIle 219
668 TCATTCACATTGTGCTTTCAGACATTCATCAAGAGCGTGCAGCGG 717
    ||||| ||||| ||||| ||||| ||||| |||||
220 ProArgThrLleuLysValSerGlnProGlyProThrArg.SerGlnProL 236
718 CTCTCTCAGGCGCTGAGCGCGCGG.....GGG 746
    ||| ||||| ||||| ||||| |||||
236 euAspGlnIlePro...GlyProSerGlnThrProSerLleuThrSer 251
747 CTGGGGTTC.....GACACCAAGCGCGG..... 770
    ||||| ||||| ||||| ||||| ||||| |||||
252 LLeuGlySerThrProLleuLleuGlnLysThrLysGlyLysLysLysLys 268
771 ..CGGCGCGCGCTTGCAGCTGAGCGCGCTGCG 800
    ||| ||||| ::::: |||||
268 uProLleuGlyLleuLleuValGlyValThrSer 278
seq_name: sp_rodent:09EPUS
  
```

```

seq_documentation_block:
ID Q9EPUS PRELIMINARY; PRT; 655 AA.
AC Q9EPUS;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE DR6..
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID-10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=KIDNEY;
RA Isogeni D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
RT (DR6)".
RI Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL:AF322069; AAC38115.1;
SQ
SEQUENCE 655 AA: 71909 MW; 1A97C1432799E4FB CRC64;

alignment_scores:                      Length:                      219
Quality:                      292.00                      Gaps:                      4
Ratio:                      2.454                      Percent Identity:                      33.333
Percent Similarity:                      54.338

Alignment_block:
US-09-006-352-1 x Q9EPUS ..

Align seg 1/1 to: Q9EPUS from: 1 to: 655

58 CTGTGCTGTGCTGTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCTGTG 107
    ||| ||||| ||| ::::: ||||| ::::: |||||
30 LeuLeuLeuLeuLysPheLeuSerThrLleuThrLleuProGlyLys 46
108 CGGAGTGCAGAAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 157
    ::::: ||||| ||||| ||||| ||||| |||||
46 sThrLeuSerLleuProGlyThrArgLysValAlaArgThrThrGly 63
158 AGCGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 207
    ::::: ||||| ||||| ||||| ||||| |||||
63 LValLeuThrCysAspLysCysProLalaGlyThrValSerGlnLys 79
208 TCCGCGCGAGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 257
    ||| ||||| ||||| ||||| ||||| |||||
80 CysThrAsnMetSerLleuArgValCysSerSerCysProLalaGlyThr 96
258 CAGCGAGTGTGAGACTGACCTGAGCGCGCGCGCGCGCGCGCGCGCTGT 307
    ::::: ||||| ||||| ||||| ||||| |||||
96 eThrArgLysGlnAsnGlyLleuLysGlnLysAspCysSerGlnProC 113
308 GCGGAGAGCGGTGAGAGAGAGCGCGCGCTTCCAGCGCGCGCGCGCG 357
    ||| ||||| ||||| ||||| |||||
113 ySPTrProMetLleuLysArgLysProCysAlaLalaLleuThrAspArg 129
358 GCGTGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 407
    ||| ||||| ||||| ||||| |||||
130 GlnCysLleuCysProProGlyMetLysLysSerAsnGlyThrCysAlaPr 146
408 GCAAGCATGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 457
    ||||| ||||| ||||| ||||| ||||| |||||
146 oHisThrValCysProValGlyThrGlyValArgLysGlyThrGlnAla 163
458 GCGAGAAACAGAGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 507
    ::::: ||||| ||||| ||||| ||||| |||||
163 sGlnLysPvalArgCysLysGlnCysAlaArgLysThrPheSerAspVal 179
508 AGCTGCAGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 557
    ||||| ::::: ||||| ||||| |||||
180 ProSerSerValMetLysCysAlaLalaHisThrAspCysLleuLys 196
  
```

```

558 CCGGCGCCATGTCAGGCGCTTCTCCCATGACACCGCTGTC... 603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
196 nleugluvallylsproglythrlysgluThrAspAsnValcysglym 213
604 .....ACAGCGCACGTGGCTCCCGCCACGCA..... 631
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
213 etargleuphpheserSerThrAsn.ProProSerSerGlyThrValTh 229
632 .....CCAGGTPACAGAGCTGAGAGTGTGAGCGCTGCGTCAT 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
229 rpheserHisProgluHisMetglu.....SerHisAspValProSers 244
672 CGACT 676
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
244 erThr 245
seq_name: sp_human:075509

```

```

seq_documentation_block:
ID 075509 PRELIMINARY; PRT; 655 AA.
AC 075509;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE TNFR-RELATED DEATH RECEPTOR-6 (DJ181J13.1) (DR6 (TNFR-RELATED DEATH
DE RECEPTOR-6)).
DR6 OR DJ181J13.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Yu G.,
RA Vincenz C., Aggarwal B.B., Dixit V.M.;
RT Identification and functional characterization of DR6, a novel death
RT domain-containing TNF receptor."
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Parker A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF068668; AAC34583.1; -.
DR EMBL: AL096801; CAB75692.1; -.
DR HSSP: P07174; INGR.
DR InterPro: IPR000488; -.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_c6; 4.
DR Pfam: PF00531; death; 1.
DR ProDom: PD000771; -. 1.
DR PROSITE: PS00017; DEATH DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS0050; TNFR_NGFR_2; 1.
DR SMART: SM00005; DEATH; 1.
KW Receptor.
SQ SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

```

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alignment_scores:
  Quality: 289.00 Length: 194
  Ratio: 2.676 Gaps: 3
  Percent Similarity: 55.670 Percent Identity: 34.536
alignment_block:
US-09-006-352-1 x 075509 ..
Align seg 1/1 to: 075509 from: 1 to: 655

```

```

127 ACCTACCCCTGGCGAGCAGACAGAGGCGGCTGTGTGGGCCCA 176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
53 Thirtyratghisvalasparalathrglycinalleutricysasply 69

```

```

177 GTGCCCCCAGGACACCTTTGTGACAGGCGCGTCCGCGGAGACAGCCCA 226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
69 scysProAlaGlyThrTyValSerGluHisCysThrAsnThrLeuA 86
227 CGAGCGTGGGCGCGTGGCCAGCCCGCCACTACACCGACTTCTGGAACTAC 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
86 rValCysSerSerCysProValGlyThrPheThrArgHisGluAsnGly 102
277 CTGAGCGCCTCCCTACTGCACAGCTCTCCGCGGAGCGTGAGAGACA 326
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
103 lIleGluTyScyHisAspCysSerGlnProCysProTyrPrometIleG 119
327 GGCACGGGCTTGCACGCCACCCACACACCGTGCCTGCCGCGCCAGCG 376
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
119 ulysLeuProCysAlaAlaLeuThrAspArgGluCysThrCysProPro 136
377 GCTTCTGCGCGCAGCGCTTCTGCTTGTGAGACAGCATCGTTCGCACT 426
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
136 lMetPheGlnSerAsnAlaThrCysAlaProHisThrValCysProVal 152
427 GTCGCGCGCGTGAATGCCCCGCGCACCCCGAGCCAGACAGCAGTGGCA 476
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
153 GlyThrGlyValArgLysLysGlyThrGluThrGluAspValArgCysLy 169
477 GCGGTGCCCCCGAGCGACCTTCTGACGACGAGCTCAGCTCAGAGCAGT 526
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
169 sGlnCysAlaArgGlyThrPheSerAspValProSerSerValMetLysC 186
527 GCGACCCCGCCAGCAGTGCAGCGCGCTGGCGCTGCGCTCATATGGCA 576
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
186 yLysAlaTyThrAspCysLeuSerGlnAsnLeuValValLysPro 202
577 GCGTCTCTCCCATGACACCGCTGTCAGCAGCTCAGCTGCGTCCCT 626
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
203 GlyThrLysGluThrAspAsnValCysGlyThrLeuProSerPheSerSe 219
627 CAGCACCGAG...GTACGAGAGCT..... 648
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
219 rSerThrSerProSerProGlyThrAlaIlePheProArgProGluHisM 236
649 ..GAGAGCTGTGAGCGCTGCGCTCATGCACT 676
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
236 etGluThrHisGlu.ValProSerSerThr 245
seq_name: sp_virus:057277

```

```

seq_documentation_block:
ID 057277 PRELIMINARY; PRT; 348 AA.
AC 057277;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1996(96-17), ZAIRE-1996 (96-16);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U88543; AAB94378.1; -.
DR EMBL: U87841; AAB94358.1; -.
DR HSSP: P25942; ICDF.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_c6; 2.
DR ProDom: PD000771; -. 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS0050; TNFR_NGFR_2; 2.
DR SMART: SM00208; TNFR; 1.
SQ SEQUENCE 348 AA; 38212 MW; 54019521556C2D8F CRC64;

```





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 31, 2001, 09:41:15 ; Search time 1618.98 Seconds  
(without alignments)  
6288.356 Million cell updates/sec

Title: US-09-006-352-1

Perfect score: 1077

Sequence: 1 gctctccctgctccgcgaag.....aaaaaaaaaaaaaaaaaaaaa 1077

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_est4:\*

5: gb\_est5:\*

6: gb\_est6:\*

7: gb\_est7:\*

8: gb\_est8:\*

9: gb\_est9:\*

10: gb\_est10:\*

11: gb\_est11:\*

12: gb\_est12:\*

13: gb\_est13:\*

14: gb\_est14:\*

15: gb\_est15:\*

16: gb\_est16:\*

17: gb\_est17:\*

18: gb\_est18:\*

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45: em\_esthum11:\*

46: em\_esthum12:\*

47: em\_esthum13:\*

48: em\_esthum14:\*

49: em\_esthum15:\*

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59: em\_esthum25:\*

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63: em\_estin1:\*

64: em\_estin2:\*

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66: em\_estin4:\*

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71: em\_estov2:\*

72: em\_estp11:\*

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76: em\_estp15:\*

77: em\_estp16:\*

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79: em\_estp18:\*

80: em\_estp19:\*

81: em\_estp110:\*

82: em\_estro1:\*

83: em\_estro2:\*

84: em\_estro3:\*

85: em\_estro4:\*

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 257: gb\_est177:\*  
 258: gb\_est178:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	ID	Description
1	656.4	60.9	879	141	BE878006
2	610.8	56.7	674	147	BF339551
3	594	55.2	617	141	BE878908
4	586.8	54.5	600	113	AW562121
5	566.6	52.6	692	111	AW083241
6	510.6	47.4	514	116	AW471140
7	496.2	46.1	540	119	AW662363
8	488	44.4	697	141	BE873766
9	478	44.3	698	143	BF001490
10	473.4	44.0	575	24	AT718743
11	449	41.7	515	111	AW083914
12	445	41.3	445	102	AI857725
13	442.6	41.1	551	141	BE879166
14	438.6	40.7	459	110	AW014771
15	437.8	40.6	453	113	AW020499
16	436	40.5	436	18	AT290210
17	418	38.8	430	22	AI561219
18	407	37.8	468	120	AW675220
19	405	37.6	405	21	AI520716
20	403.8	37.5	467	1	AA025673
21	401.2	37.3	417	110	AW006931
22	398.6	37.0	554	116	AW646298
23	381.8	35.5	388	151	BE591174
24	379.6	35.2	452	120	AW771720
25	366	34.0	406	22	AI624643
26	363	33.7	399	111	AW080544
27	346.4	32.2	378	9	AAI63366
28	346	32.1	358	18	AI282851
29	325.6	30.2	344	17	AI185297
30	318	29.5	423	111	AW083605
31	306.6	28.5	461	11	AA740147
32	289.2	26.9	413	114	AW272130
33	282.4	26.2	340	114	AW316995
34	271.2	25.2	295	120	AW801019
35	271	25.2	271	141	BE877829
36	270	25.1	310	190	M67560
37	260.6	24.2	428	3	AAI55701
38	258.8	24.0	273	103	AI910466
39	256	23.8	378	19	AI380034
40	253.4	23.5	266	9	AA577603
41	253.4	23.5	285	9	AA603704
42	253.4	23.5	358	111	AW080904
43	247.6	23.0	265	8	AA514270
44	242.2	22.5	283	3	AAI55646
45	241	22.4	241	20	AI446656

## ALIGNMENTS

RESULT	1
LOCUS	BE878006
DEFINITION	BE878006 679 bp mRNA EST 20-OCT-2000 6014d9774ef1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891908 5', mRNA sequence.
ACCESSION	BE878006
VERSION	BE878006.1 GI:10326782
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 679) NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> . National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999) Contact: Robert Strausberg, Ph.D.
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Email: c9apb5-r@mail.nih.gov  
Tissue Procurement: DCTP/DRP/Gazdar  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLNA9677 row h column: 21  
High quality sequence stop: 672.  
Location/Qualifiers

## FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1fb="IMAGE:3891908"
/clone_1lb="Nrl_MGC_69"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dT."
Average insert size 1.1 kb. Library constructed by Life
Technologies."

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Query Match 60.9%; Score 656.4; DB 141; Length 679;

Best Local Similarity 99.8%; Pred. NO. 2,35e-126;  
Matches 657; Conservative 0; Mismatches 1; Indels 0; Gaps 0

348 ccaacaacgtgctgcgcgcgtgcgcgaacgcggtcttcttcgcgcgaacgctggttctctgttga 407

11 CCACACCGCTGCGGCTGCCGACCGGCTTCTTGGCGACGCTGGTTTCGTTGSA 70

408 gcaagcattcgttccacctgtgcccgcgtgatgtccccggcaccgccagccagaaac 467

71 GCACGCATCGTGTCCACCTGGTCCGGCGTCATTTGCCCCGGGGACACCCCGACCCAGAC 130

468 gcaatgccaagccgtgcgccccaagcacctctcagccaagcagctcagctcagagcagtg 527

b

131	GCAGTGGCCAGCGCGTGGCCCCCCCAAGGCACTTCTCAGCCAGCAGCTTCAGACTCAGAGCAGTG	190
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528 ccagcccccacgcgaactgcacgcgcctgggcctgcgcctcaatgtgcaggtcttcctc 587

191 C G A G C C C A C C G C A A C T G C A C G G C C T G G C C T G G C C C T C A A T G T G C C A G G C T T T C T C 250

588 ccataacacctgtgcaccagctgcactgcttccccctcagcaccaggttaccagagc 647

b

251	CCATGACACCCCTGTGGCACCAGCTGCACCTGCTTCCCCCTCAGCACCAGGGTACCAAGAGC	310
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648 ttgaggagttgtacgcgttcgcgtcatcgcacttctgttgcttcagagacatctccatcaagag 707

b  
311 TGAGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAG 370

708 gctgcagcgcgtctgtcagagccctcgagccccgagaggttgggtccgacaccaaagc 767

371 GCTGCAGCGGCTGCTGCAGGGCCCTTCGAGGCCCGGAGGGCTGGGGTCCGACACCAAGGCG 430

768 gggccgcgcgcgccttcagctgaagctgcgtccgcgcgcgtcaacgagagctcctcctggggcgca 827

431 GGGCCGGCGGCGCTTGCAGCTGAGCTGGCTGGCGGCTCAGGAGCTCTGGGGCGCA 490

828 ggaacgggcgcctgctggtgcgcgtcgtcacggcgcctgcgcgctggccacgagatccccggct 887

b 491 GGACGGGGCGCTGCTGTTGCGGCTGCTGCAGCGCTGCGCGTGGCCAGCATGCCCCGGCT 550

888 ggagcgcgagcgtccgcgttagcgccttcctccctgtgcaactatcctgccccctctattta 947

551 GGAGCGAGCGTCCGTCGAGCGGCTTCCTCCCTGTGACACGATCCTGGCCCCCTCTATTTA 610

348 ttctacatccttgcgcacccacttgcactgaagaagcgtttttttaaataagaagaa 1005

611 TTCTACATCCTTGGGACCCACCTTGCACCTGAAGAAGAGGCTTTTAAATAGAGAAA 668

RESULT 2  
LOCUS BF339551 874 bp mRNA EST 22-NOV-2000  
DEFINITION 602039016P1 NCI.CGPB\_Brn64 Homo sapiens cDNA clone IMAGE:4186995  
ACCESSION BF339551  
VERSION BF339551.1 GI:11286006  
KEYWORDS EST  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 874)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE NIH-MGC http://mgc.nci.nih.gov/  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM9508 row: P column: 04  
High quality sequence stop: 701.  
Location/Qualifiers  
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/clone="IMAGE:4186995"  
/clone\_lib="NCI.CGPB\_Brn64"  
/tissue\_type="glioblastoma with EGFR amplification"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site:1; NotI;  
Site:2; SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.57 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 129 a 299 c 301 g 145 t  
ORIGIN  
Query Match 56.7%; Score 610.8; DB 147; Length 874;  
Best Local Similarity 89.6%; Pred. No. 7.6e-117;  
Matches 679; Conservative 0; Mismatches 77; Indels 2; Gaps 2;

361 tgcgcctgcgcagaccgagcttcttcgcagacagcttgatttcgttggagagacagatcgtgtc 420  
|||||  
Db 434 TGCCCGTGCCTGCACCGGCTTCTTCCGCGACGCTGGTTCCTGGAGACGACATCGTGT 493  
|||||  
Qy 421 ccaactgtgtgcgcgagtgatattgcccgggagacccccagcagaaacagcagtgcacgcg 480  
|||||  
Db 494 CCACTGTGTCGGGCGGTATGTCGCCGGACCCCAAGCAGACACGAGGCGT 553  
|||||  
Qy 481 tgcgccccagcagcttcttcagcagacagcttcagctcagagcagtgccagccacccgc 540  
|||||  
Db 554 GCCCCAGGCAACCTTCCAGCCAGACAGCTCCAGCTCAGACAGTGCACGCCACCG- 612  
|||||  
Qy 541 aactgcagggccttgagccttgccctcaatcgtgcagagcttcttcctccatgcaccccg 600  
|||||  
Db 613 AACTGCACGCGCTGGGGGCTGCGCTCCCAATGTCGAGGCTCTCCATGACACCCCTG 672  
|||||  
Qy 601 tgcacagctgcagctgtctcccttcagcagacaggttacccagagctgcagagtgtag 660  
|||||  
Db 673 TGCCACACACTCACTGCTTCCCTCCAGCA-CAGGGTACAGAGTGTATGATGATGAG 731  
|||||  
Qy 661 cgtgcgcatacgaattgtgtgtcttcacagagacatccatcaagagctgcagcgctg 720  
|||||  
Db 732 CGTCCGCTCTCTGTGAGTTGTGGCTTCCAGGACTCTCCATCAAGAGGTCGGTGGG 791  
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Qy 721 ctgcagggccttcagggcccgagagctgcggcgac 758  
|||||  
Db 792 GCCTTAGCCCGAGGTGGGTCCGCCAGGGGGCGGC 829  
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RESULT 3  
LOCUS BE878908 617 bp mRNA EST 20-OCT-2000  
DEFINITION 601492609P1 NIH\_MGC\_69 Homo sapiens cDNA clone IMAGE:3894794 5',  
mRNA sequence.  
ACCESSION BE878908  
VERSION BE878908.1 GI:10327684  
KEYWORDS EST  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 617)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE NIH-MGC http://mgc.nci.nih.gov/  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF/Gazdar  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM9685 row: a column: 03  
High quality sequence stop: 617.  
Location/Qualifiers  
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/clone="IMAGE:3894794"  
/clone\_lib="NIH\_MGC\_69"  
/tissue\_type="large cell carcinoma, undifferentiated"  
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/note="Organ: lung; Vector: pCMV-SPORT6; Site:1; NotI;  
Site:2; SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.1 kb. Library constructed by Life  
Technologies."  
BASE COUNT 91 a 224 c 203 g 99 t  
ORIGIN  
Query Match 55.2%; Score 594; DB 141; Length 617;

Best Local Similarity 99.8%; Pred. No. 2.3e-113;  
Matches 605; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 267 ctggaactactgagagcgtcgcctactgcaacgtctctgagggagcgtgagga 326  
Db 3 CTGGAATCTACTGAGGCGTCCCTACTGCAAGTCTCTGCGGAGCCTGAGAGA 62  
Qy 327 ggaacgggtctgcacgcacacacacacgltgcctgcgtctgcacacggtctctgc 386  
Db 63 GGCACGGGCTTGGACGACCCACCAACCGTGCCTGCGCTGCGGACCGCTTCTGCG 122  
Qy 387 ggaacgtggttctgcttgtagcagcagcatggttccacccgtggtgcggtgtatgcc 446  
Db 123 GCACGGCTGTTTCTGCTTGGAGCAGCATGCTGTCACCTGTCGCCGCGGATTTGCC 182  
Qy 447 gggacccccagacacacacacacacagtcacagcgtgcacacacacacacacacac 506  
Db 183 GGGCAGCCCCAGCAGACACGACAGTCCAGCCTGCCCCAGGACCTTTCTAGCCAG 242  
Qy 507 cagctcagctcagagcagtcgacagcccaacacacacacacacacacacacacacac 566  
Db 243 CAGCTCAGCTCAGAGCAGTGCAGGCGCCACCGCACTGCACGGCCCTGGGCTTGGCCCT 302  
Qy 567 caatgtgcagcgtctctctccatgacacccgtgtgacacacacacacacacacacac 626  
Db 303 CAATGTGCCAGGCTCTTCTTCCATGACACCTCTGTCACACAGCTGACCTGCTCCCT 362  
Qy 627 cagcaccagagtcacacagacacacacacacacacacacacacacacacacacacac 686  
Db 363 CAGCACCAGGCTTACACAGACCTGAGAGTGTGAGCGTGCCTGTCATGACATTTTGGCTTT 422  
Qy 687 cagagacatctcactcaagagcgtcagcagcgtctgacagccctcagagcccccagag 746  
Db 423 CAGAGACATCTCCATCAAGAGGCTGACGCGCTGCTGACGCGCTTCAGGCGCCGGAGG 482  
Qy 747 ctgggtctgcac 806  
Db 483 CTGGGGTCCACACACAGGCGGCGCGCGCTTGCACCTGAACTGCGTCCGCGCT 542  
Qy 807 cagagac 866  
Db 543 CAGGAGACTCTCTGGGGCGGACGAGACGGGCGCTGCTGCTGCGG-TGCTGCAGGCGCTGCG 601  
Qy 867 cgtgagc 872  
Db 602 CGTGGC 607

RESULT 4  
AM262121/c 600 bp mRNA EST 28-DEC-1999  
LOCUS xg31d04.x1 NCI-CGAP Lu28 Homo sapiens cDNA clone IMAGE:2752231 3'  
DEFINITION similar to TR:095407 095407 DECOY RECEPTOR 3.; contains TARI. b1  
TARI repetitive element; mRNA sequence.

ACCESSION AM262121 GI:6638937  
VERSION AM262121  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 600)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D. CDNA Library Preparation: Life  
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The  
I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.lnl.gov/db/rp/image/image.html

Possible reversed clone: polyT not found  
Seq primer: -40UP from Gibco  
High quality sequence stop: 410.  
Location/Qualifiers

FEATURES

source 1. 600  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_id="IMAGE:2752231"  
/clone\_lib="NCI-CGAP\_Lu28"  
/tissue\_type="two pooled squamous cell carcinomas"  
/lab\_host="DH10B"  
/note="organ: lung; Vector: pCMV-Sport6; Site: 1; Salt:  
Site: 2; NotI. Cloned unidirectionally. Primer: oligo dt.  
Library constructed by Life Technologies."  
BASE COUNT 120 a 177 c 199 g 102 t 2 others  
ORIGIN

Query Match 54.5%; Score 586.8; DB 113; Length 600;  
Best Local Similarity 98.5%; Pred. No. 7.1e-112;  
Matches 591; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 445 ccgggacccccagac 504  
Db 600 CCGGAGCAGCCAGCCAGCAGACAGTGCAGCGCGTGCCTGCGGACCTTTCTAGCC 541  
Qy 505 .agcagctcagctcagacagcgtcagcagcccaacacacacacacacacacacacacac 564  
Db 540 AGCAGCTCAGCTCAGAGAGTGCAGCGCCACCGCACTGCAGGCGCGGCGGCGGCGG 481  
Qy 565 ctcaatgtgcagcgtctctctccatgacacccgtgtgacacacacacacacacacacac 624  
Db 480 CTCAATGTGCCAGGCTCTTCTTCCATGACACCTGTGTGACACAGCTGACCTGCTCC 421  
Qy 625 ctacagac 684  
Db 420 CTCAGCAGCAGGATACAGAGAGTGTAGAGTGTAGAGTGTAGAGTGTAGAGTGTAGAG 361  
Qy 685 ttccagac 744  
Db 360 TTCAGAGACATCTCCATCAAGAGGCTGAGGCGCTGCTGAGCGCTTCAGGCGCCGAG 301  
Qy 745 ggcgtgggtccgac 804  
Db 300 GGCCTGGGCTCCGACACCAAGGCGGCGCGCGCTTGCAGCTGAAGCTGCTGCGCGG 241  
Qy 805 ctacagagac 864  
Db 240 CTCAGGAGCTCTGCGGCGGCGGCGGCGGCGCTGCTGAGGCGCTGCTGAGGCGCTG 181  
Qy 865 ccgctgac 924  
Db 180 CGCGTGGCGCAGAGATGCCGCGGCTGAGCGGAGCGTCCGTGAGCGCTTCTGCTGAGC 121  
Qy 925 tgatcctggccctctatattctacatccttgcacccacacacacacacacacacacac 984  
Db 120 TGATCCTGGCCCTCTTATTATTATTAATCAATCTTGGCAGCCCACTTGCACTGAAGAG 61  
Qy 985 ctttttttaataagaagaatagagtttcttaagctatttttaagaagcttttcat 1044  
Db 60 CTTTtttttaataagaagaatagagtttcttaagctatttttaagaagcttttcat 1

RESULT 5  
AM083241/c 692 bp mRNA EST 14-OCT-1999  
LOCUS xc07a04.x1 NCI-CGAP Co21 Homo sapiens cDNA clone IMAGE:258534 3'  
DEFINITION similar to TR:095407 095407 DECOY RECEPTOR 3.; contains L1.b1  
repetitive element; mRNA sequence.

ACCESSION	AM083241
VERSION	AM083241.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini, Homnidae: Homo. 1 (Bases 1 to 692)
AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@bbs-remail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Chrisa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
FEATURES	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://www.bio.llnl.gov/bbrp/image/image.html">www.bio.llnl.gov/bbrp/image/image.html</a> Seq primer: -400p from G1pco High quality sequence stop: 414.
SOURCE	1..692

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2583534"
/clone_1id="NCI CGAP C021"
/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/notes="Organ: colon; Vector: PCMV-SF0RT6; Site_1: SalI; Site_2: NciI; Cloned unidirectionally. Primer: Oligo dr. Normalized to Cot >500. Average insert size 1.04kb. Normalized version of NCI-CGAP-Col8. Library constructed by Life Technologies."

```

Query Match	52.6%;	Score 566.6;	DB 111;	Length 692;
Best Local Similarity	97.9%;	Pred. No. 1.1e-107;		
Matches 605; Conservative	0;	Mismatches 10;	Indels 3;	Gaps 3;

QY	404	tggagacagcatcgtgtccaccctgtgtgcggagcgtgattgtcccgcgacccccagcaga	463
Db	619	TGGAGCAGCATCGTGTCCACTT-GTGGCGGCGTGATTGTCGCCGGCACCCAGTGCAGA	561
QY	464	acacagcagtggtccagccggttccccccaggacattctcagccagaagctccagctcagagc	523
Db	560	ACACGCAAGTCCAGCCGCTGCCCCCNAGGACACTTCTCAGACACCACTCCAGTCCAGACC	501
QY	524	agtgccagcccccccgcaactgcacgagccctcggggccctgcgcccacatgtgtccagctctt	583
Db	500	AGTGGCAGCCCCACCCCAACTGCAGGGCCCTGGGGCCCTCAATATGTCCAGGCTATT	441
QY	584	ccctcccatgacacccctgtgtcacagctgcatactgtcttcccccctcagacacaggtaccag	643
Db	440	CTTCCCATGATCACCCCTGTGTACACACTGTCACTATGGCTTCCCCCTACACACAGGATACAG	381
QY	644	gaagctaaaggaagtgtagcgtgtgcgttcatactgaatttgtgtcttcagagacatctcatca	703
Db	380	GACCTAGAGGAGTGTGAGCTGGCCGTCATCAGCACTTGTGTGGCTTCCAGACATCTCCATCA	321
QY	704	agagagcttgcaagcagctctgcctgcagagcccttcagagccccggaggagctaggaatccgaaccaa	763
Db	320	AGAGGCTGCACAGGGCTGTGTGAGGCCCTCGAGGCCCGGAGGGCTGGGGTCCGACACCA	261
QY	764	ggagcgggacgcgcgcgccttgacagctgaaagc-tgctgtggaggtctcagagctcagctccggag	822
Db	260	GGGCGGGCGCGCGGCTTGTGACGTGAANACTTGGTGGCGGGCTCACGGAGCTCTCGGGG	201

QY	823	gacgaagacggggcgctgcctgcgtgcgtgcctgcgaagcgctgcgcgtgcgccagatagccc	882
Dp	200	gcccacagacggggccctctctctctcgcctcgcctcgcacagccctccgcgcgagccagatagccc	141
QY	883	gggcctgcgagcgagcgctcgcgtgcgcctctccctcctgcgaactgcctcgcgcctctt	942
Dp	140	ggcctctgcacccggagggctccggagacggcttctccctcgtgcactgactcctggccccctct	81
QY	943	attattctacatcctctgcgaccccaactgcgaactgcgaagagcgcctttttttaaataagaa	1007
Dp	80	attttattttacacatctcttgccaccccaactgcgaactgcgaagagcctttttttaaataagaa	21
QY	1002	gaaatgaggttttcttaaa	1019
Dp	20	gaatgagcgttttcttaaa 3	

RESULT	6
LOCUS	AM471440/c
DEFINITION	AM471440 540 bp mRNA EST 24-FEB-2000
ACCESION	xw59506.x1 NCI_CGAP_Pan1 Homo sapiens CDNA clone IMAGE:2632322
VERSION	similar to :tr:095407 095407 DECOY RECEPTOR 3. ; contains TAR1.b
KEYWORDS	TAR1 repetitive element ; mRNA sequence.
SOURCE	AM471440.1 GI:7041546
	EST.
	human.

ORGANISM	Human sapiens
Home	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
NCBI	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	NCI-CGAP n14p / 2404 nci.nih.gov/ncicgap
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
TITLE	Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Life Technologies catalog #: 11548-013  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information [www.bio.11nl.gov/bdbp/image/image.html](http://www.bio.11nl.gov/bdbp/image/image.html)  
found through the I.M.A.G.E. Consortium/LNL, at:  
www.bio.11nl.gov/bdbp/image/image.html  
Seq primer: -40UP from Gibco  
High quality sequence stop: 387.

FEATURES	
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location/Qualifiers	
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/organism="Homo sapiens"	
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/note="Organ: pancreas; Vector: pCMV-SPOrM6; Site:1: S Site_-2: NotI; Cloned unidirectionally. Primer: Oligo Average insert size 1.72 kb. Life Technologies catalog 11548-013"	
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165 c	
160 g	
88 t	
7 others	
BASE COUNT	
BRIGIN .	

Query Match	47.4%	Score 510.6	DB 116	Length 540
Best Local Similarity	96.1%	Pred. No. 4,6e-96		
Matches 519	Conservative	0	Mismatches 21	Indels 0
			Gaps	
QY 484	ccccccagcagcctcttcagcagcagccttcagcagcagtcgcagcccccacgcac	543		
DB 540	ccctttggagacattcttcagcagcagccttcagcagcagtcgcagcccccacgcac	481		
QY 544	tgcacgccccttggagccttgcacccaatgtgcagcgtcttcctccatgacacctgtgc	603		
DB 480	tgtatggcccttggagccttgcacccaatgtgcagcgtcttcctccatgacacctgtgc	421		
QY 604	accacgtcgcacatgagcttcctcccttcagacacacagaggtaccacagagcttgagaggt	663		

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Db 420 ACCAGNATGCTGGCTTCCCCCTCAGCACACAGGTTACAGAGCTGAGAGTGTGAGCGT 361
QY 664 gccatcatcacttctgtgtcttccagagacatctccatcaagaagctcagcgctctgt 723
Db 360 GCGGTATGACACTTGTGTGCGTTTCAGAGCATCTCCATCAAGAGCGTGCAGCGGCTCTG 301
QY 724 caggccctcgaagcccccgaaggctggtgtcgaacacaaaggcgcgcgctctg 783
Db 300 CAGGCCCTCAGAGCCCCGAGGCGCTGGCGTCCGACACCAAGGCGGCGCGCCCTCTTG 241
QY 784 caactaagtgctgcggcgctcagaagctctctgtgggacgaggaacgggagctgtg 843
Db 240 CAGCTGAAGCTGCTGCGCGGCTCAGCGAGCTCTTGCGGCGAGCGAGCGGCGCTG 181
QY 844 gtgcgctgtcgaagcgctgcgctgtgccaagatgcccgagctgagcgagcgtcgt 903
Db 180 GTGCGGCTGTGACAGGCGCTGCGCGTGGCCAGATGCCCGGCTGAGCGAGCGTCCGT 121
QY 904 gagcgcttcctcctgtgcaatgacatcctgccccctctatctatctacatccttgca 963
Db 120 GAGCGCTTCTCCCTGACGACTGATCCGCGCCCTCTATTATCTACATCCTTGCA 61
QY 964 ccccgcttgcacggaagagcttttttaataagaagaatgaggttctctaaagct 1023
Db 60 CCCACTTGACATGAAGAGGCTTTTAAATAGAAAGATGAGGCTTTAAAGCTT 1

RESULT 7
AM662363/c 514 bp mRNA EST 06-APR-2000
LOCUS h123f01.x1 NCI-CGAP.Col4 Homo sapiens cDNA clone IMAGE:2973337 3'
DEFINITION similar to TR:095407 095407 DECOY RECEPTOR 3.; contains TAR1.b1
TAR1 repetitive element ;, mRNA sequence.
ACCESSION AM662363
KEYWORDS EST.
SOURCE AM662363.1 GI:7454901
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 514)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/resources.shtml
Seq primer: -400P from Gibco
High quality sequence stop: 368.
Location/Qualifiers
1..514
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2973337"
/clone.lib="NCI.CGAP.Col4"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: PCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"

BASE COUNT 113 a 156 c 159 g 85 t 1 others
ORIGIN
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Query Match 46.1%; Score 496.2; DB 119; Length 514;
Best Local Similarity 99.0%; Pred. No. 4, 5e-93;
Matches 509; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 532 cccacgcgaactgcagagccctgggcttgccttaattgcaggtcttctccat 591
Db 514 CCCACAGCAACTGCACAGGCGCTGGGCGCTGACCTCAATATGACGAGCTCTTCCAT 455
QY 592 gacacctgtgcaacaagctcaactggtctccctcagaacaaaggatcagaagctgag 651
Db 454 GACACCTGTGTGACACAGCTGACTGTGCTCCCTTCAGACACAGGATACAGAGCTGAG 395
QY 652 gaagtgaagcgtgcgcgtcagctcagacttgtgtcttccagagacatctcatcaagaagctg 711
Db 394 GAGTGTAGCGGTGCGCCTCAATGAGACTTGTGTGCTTCCAGAGCAATCTCCATCAAGAGCTG 335
QY 712 cagcgctgtctgcagagcctcagagcccggaaggtcgtgggtctcgacacaaaggcgagc 771
Db 334 CAGCGGCTGTGACAGGCGCTTGAAGCCCGAGGCGCTGGGCTCGACACCAAGGCGCGGC 275
QY 772 cgcgcgccttgcaagctgaaagctcgtcgcgcgtcgaagctcctcgtgggagcgagac 831
Db 274 CGCGGCGCTTGCAGCTGAGACTGCTGCGGCTCAGCGAGCTCTGAGGCGCAGAGC 215
QY 832 gggcgctgtcgtgctgcgctgtgcagagcgctgcgcgtgcgctgcgagatgcccgagctgag 891
Db 214 GGGCGCTGTGCGTGGCGCTGCTGACAGGCGCTGCGGCTGCGGCGAGAGTCCCGGCTGAG 155
QY 892 cggagcgctcgtgagagcttccctgtgcaatgacatcctgccccctatattct 951
Db 154 CGGAGCGCTCGTGTGAGCGCTTCTCCCTGTGCTGACATGATCGGCGCTCTTATTATTC 95
QY 952 acatccttgcaacccactgcactgaagaaggt-ttttttaagaagaataggt 1010
Db 94 ACATCTTGGACACCCGACTTGACATGAGAGGCTTTTAAATAGAAAGATGAGG 35
QY 1011 ttcttaagcttatttataaagcttttcat 1044
Db 34 TTTCTTAAGCTTATTATTAAAGCTTTTTCAT 1

RESULT 8
BE873766 697 bp mRNA EST 20-OCT-2000
LOCUS 601483915F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886635 5',
DEFINITION mRNA sequence.
ACCESSION BE873766
KEYWORDS EST.
SOURCE BE873766.1 GI:10322542
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 697)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM963 row: m column: 04
High quality sequence stop: 675.
Location/Qualifiers
1..697
/organism="Homo sapiens"
/db_xref="taxon:9606"

FEATURES
source
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/clone="IMAGE:3886635"
/issue="large cell carcinoma, undifferentiated"
/lab_host="DHI08 (Phage-resistant)"
/note="Organ: lung; Vector: PCMV-SpO6; Site: 1; Not:
Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT 112 a 245 c 224 g 115 t 1 others
ORIGIN
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Query Match 45.3%; Score 488; DB 141; Length 697;
Best Local Similarity 92.8%; Pred. No. 2.3e-91;
Matches 567; Conservative 0; Mismatches 36; Indels 8; Gaps 5;
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OY 1 gctctccctgctccagcaagaccatgagggcgctgaggaagcgagcctgtcgtctg 60
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Db 55 GCTCTCCCTGCTCCAGCAAGACCATGAGGGCTTGAGGGCCAGGCTGTCTCTCTG 114
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OY 61 tgcctgtgttgagcgtcctgctgctgctgctgctgctgctgctgctgctgctg 120
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Db 115 TGCTGTGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 174
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OY 121 aacccacactacccctgagcgagacagagagagagagagagagagagagagagag 180
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Db 175 ACACCACTACCTCTGAGGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234
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OY 181 ccccgagcacttctgagcgagcgctgagcgagcgagcgagcgagcgagcgagcgag 240
|||||
Db 235 CCCCAGGACCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 293
|||||
OY 241 tgcacagcgagcacttctgagcgagcgctgagcgagcgagcgagcgagcgagcgag 300
|||||
Db 294 TGTCACCGCGGCACTACACGCACTGCTGAGACTGCTGAGAGAGAGAGAGAGAGAG 353
|||||
OY 301 gtctctgagagagcgagagagagagagagagagagagagagagagagagagagag 360
|||||
Db 354 GTCTCTGCGGGAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 411
|||||
OY 361 tgcagctgagcagcagcgtctctgagcagcagcgtctctgagcagcagcagcagc 420
|||||
Db 412 TGCCG-TGCCGACCGGCTTCTGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 470
|||||
OY 421 ccaacctgtgagcgagcgatctgagcgagcgagcgagcgagcgagcgagcgagcgag 480
|||||
Db 471 CCACCTGGTGGCGGATGATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 530
|||||
OY 481 tgcggcgagcagcctctgagcagcagcagcagcagcagcagcagcagcagcagcag 540
|||||
Db 531 TGCCCGCCAGGACCTTCTGAGCAGAGCTCCAGCTCAAAAGACTGACAGGCCAGCG 589
|||||
OY 541 aactgagcgagcctgagcgagcagcagcagcagcagcagcagcagcagcagcagc 600
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Db 590 -AATGACGCGC--TGCGCTGCGCTCAATGTGCGAGGTCTCTCTCCATGAAACCTGTG 646
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OY 601 tgcacagcgtg 611
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Db 647 CACAGCTGATG 657
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RESULT 9
BF001490/c 478 bp mRNA EST 06-OCT-2000
LOCUS 7988h10.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:3313603 3'
DEFINITION similar to contains PRR5, b1 TARI repetitive element ;, mRNA
sequence.
ACCESSION BF001490
VERSION BF001490.1 GI:10701765
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 478)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck, M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
infoimage.llnl.gov  
Seq primer: -40bp from Glibco  
High quality sequence stop: 419.

FEATURES  
source  
location/Qualifiers

1..478  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="3313603"  
/clone\_lib="NCI\_CGAP\_Col6"  
/issue\_type="colon tumor, RER+"  
/lab\_host="DHI08"  
/note="Organ: colon; Vector: p7T3D-Pac (Pharmacia) with a  
modified polylinker; Site: 1; Not 1; Site: 2; Eco RI;  
Plasmid DNA from the normalized library NCI\_CGAP\_Col6 was  
prepared, and ss circles were made in vitro. Following HAP  
hybridization, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(clonids 1057416-1061255, and 1144584-1145351).  
Subtraction by Bento Soares and M. Fatima Bonaldo. "

```
BASE COUNT 108 a 146 c 144 g 80 t
ORIGIN
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Query Match 44.4%; Score 478; DB 143; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7e-89;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 566 tcaatgtgcagcgtcttcctccatgacacccctgagcagcagcagcagcagcagcagc 625
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Db 478 TCATGTGCGCAGGCTTCTCTCCATGACACCCCTGACACACCTGCTGCTGCTGCTGCT 419
|||||
OY 626 tcagacacaggttacacagacagcagcagcagcagcagcagcagcagcagcagcagc 685
|||||
Db 418 TCACGACAGGCTACGAGAGCTGAGAGGTGAGCTGAGCTGAGCTGAGCTGAGCTG 359
|||||
OY 686 tcaagacatctccatcaagagagcgtgacagcagcgtgacagcagcgtgacagcagc 745
|||||
Db 358 TCACGACAGGCTTCTCCATCAAGAGGCTGACGCGCTGCGAGGCGCTTCGAGGCGGAGG 299
|||||
OY 746 gctggggtccgagacacaaaggcgagcgagcgagcgtgacagcagcgtgacagcagc 805
|||||
Db 298 GCTGGGCTCCGACACCAAGGGGGGCGCGGGGCGGCTTGCAGCTGAAGCTGCGCGCGC 239
|||||
OY 806 tcaagagcctctgagggcgagcagcagcagcagcagcagcagcagcagcagcagcag 865
|||||
Db 238 TCACGACAGGCTTCTGGGGGCGGAGGAGGCGGCGGCTGCTGCTGCTGCTGCTGCTG 179
|||||
OY 866 gctgagcagagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 925
|||||
Db 178 GCGTGGCCAGAGATGCGCGGCGGCTGAGCGAGACGCTGAGCGCTGCTGCTGCTGCTG 119
|||||
OY 926 gatccctggccctcttatctatctatctatctatctatctatctatctatctatctat 985
|||||
Db 118 GATCTGAGCCGCCCTCTATTATTCTTCAATCTTGGAGACCCCACTGACGTAAGAAAGGCG 59
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OY 986 ttttttaataagaagaatgaggttcttaagcttttttaagcttttttaagctttttta 1043
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Db	58	TTTTTTTAAATAGACAAATGAGTGTTCTTAAGAAGCTATTATTTTATGAAGCTTTTCA	1
RESULT	10	A1718743	475 bp mRNA EST 10-JUN-1999
LOCUS		A1718743/c	
DEFINITION		aa95h04.xl Barstead aorta HPLRB6 Homo sapiens	cDNA clone
ACCESSION		IMAGE:2353399	3', mRNA sequence.
VERSION		A1718743	
KEYWORDS		EST.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE		1 (bases 1 to 475)	
JOURNAL		Hillier, L., Allen, M., Bowles, J., Dubugue, T., Geisel, G., Jost, S.,	
COMMENT		Kilman, D., Kucba, T., Lucy, M., Le, N., Lennon, G., Morra, M., Martin	
		White, Y., Wyllie, T., Waterston, R. and Wilson, R.	
		Washington University School of Medicine	
		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
		Tel.: 314 286 1800	
		Fax: 314 286 1810	
		Email: est@watson.wustl.edu	
		This clone is available royalty-free through LNL ; contact the	
		IMAGE Consortium (info@image.lnl.gov) for further information.	
		Seq primer: -40UP from Gibco	
		High quality sequence stop: 467.	
FEATURES		Location/Qualifiers	
source		1..475	
		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:2353399"	
		/clone_id="Barstead aorta HPLRB6"	
		/sex="male"	
		/dev_stage="adult, age 64"	
		/lab_host="DH10B (phage resistant)"	
		/note="Organ: aorta; Vector: pTR73D-pac (Pharmacia) with a	
		modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st	
		strand cDNA was primed with a Not I - oligo(dT) primer [5'	
		TGTTCACCATCTGCAAGTGGAGCGCCGCCCTTTTCTTTTCTTTTCTTTTCTTTT	
		3']; double-stranded cDNA was ligated to Eco RI adaptors	
		[5' AATTGCATGAC 3' and 5' GTTGGATCGC 3'] digested	
		with Not I and cloned into the Not I and Eco RI sites of	
		the modified pTR73 vector. Library constructed by Bob	
		Barstead."	
BASE COUNT		98 a 153 c 151 g 73 t	
ORIGIN			
Query Match		44.0%; Score 473.4; DB 24; Length 475;	
Best Local Similarity		99.8%; Pred. No. 2.4e-88;	
Matches 474; Conservative %		0; Mismatches 1; Indels 0; Gaps 0;	
Y	542	actgacagcgccctggcgtgcgttcgaatgfgccaggtcttccctcatgacacctgt	601
D	475	actgacaggccccctggccccttgaccctcaattgaccaggcctttccatgacacgctgt	416
Y	602	gcacacagtctgactgtctcccccctcaacacagaagtatcacaggagcttagagtgagc	661
D	415	gcacacagtctgacatggtctcccccctcacacacagsgtgtaccagacgttagagtgtagc	356
Y	662	gtgcgccatcgcgaacttgtgtgcttccagagaatctcatcaaagagcttgcaagcggctg	721
D	355	gtgcccgtcatcgacattgtgtgctttccaggacacattctcatcaagagcctgcacgctgc	296
Y	722	tgcagagccttgagagcccccgagaggtctgtgtgtccgaaccaagggcggcgcgagctt	781
D	295	tgcagagccttgagagcccccgagaggtctgtgtgtccgaaccaagggcggcgcgagctt	236

QY	782	tcgaactaaagctcgtctcgcgccgaaggagctcccttg99gcgcgaagcgggacgcgcgc	841
Db	235	TGCAGCTAAAGCTGCTGCTGGCGGCTCACAGGAGCTCTCTGGGGGCGAGCAGCGGGCGCTGC	176
QY	842	tgtatgcgctcgtcgcgaagcgtcgcgcgtgcgcagagatgcccg99cttg9agcgaagcgtcc	901
Db	175	TGCTGCGGCTGCTGAGGCGCTGGCGCGTGGGCGAGGATGCGGGGCTGGAGGAGCGTCC	116
QY	902	gtgagcgcttcctccctcgtgtgcaatgattccctggcccccttattatctcatccttgg	961
Db	115	GTGACCGCTTCTCCCTCTGCACTGATCTCTGGCCCCCTTATTATTCTATCTATCTTGG	56
QY	962	caccccaactgcacgcgaagagcgcttttttaaaatgaagaaatgaagttctt	1016
Db	55	CACCCCACTTGCACTGAAGAGCGCTTTTATTAATGAAGAAATGAGGTTTCTT	1
RESULT	11		
LOCUS	AM083914/c		
DEFINITION	AM083914	515 bp mRNA	EST
ACCESSION	AM083914		14-OCT-1999
VERSION	AM083914.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 515)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILMIL at: www-bio.ljml.gov/bdnp/image/image.html		
	Seq primer: -40up from Gibco		
	High quality sequence stop: 355.		
FEATURES	Location/Qualifiers		
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	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2585330"		
	/clone_1lp="NCI-CGAP-Co19"		
	/tissue_type="moderately differentiated adenocarcinoma"		
	/lab_host="DH10B"		
	/note="Organ: colon; Vector: PCMV-SPO76; Site: 1; Salt: Site: 2; Notti: Cloned unidirectionally. Primer: Oligo dT. Normalized to Cot 50. Average insert size 1.32kb. Normalized version of NCI-CGAP-Co18. Library constructed by Life Technologies."		
BASE COUNT	102 a 160 c 158 g 94 t	1 others	
ORIGIN			
Query Match	41.7%; Score 449; DB 111; Length 515;		
Best Local Similarity	95.5%; Pred. No. 2.8e-83;		
Matches 483; Conservative 0; Mismatches 21; Indels 2; Gaps 2;			
QY	514	agctcagagcagctgcgaagccacccacgcagcgcgaagcgcctgcgcgtcgcctcaatg	573
Db	515	AGCTTAGAAGCAGCTGACGCCCCCGCAANANTGCCGCGCTTGCGGCTGAGGCCCTCAATGTG	456
QY	574	ccaagctcttcctccatgacacccctgtgacacagctgtaactgtgttcctccctcaagcacc	633

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|||||
Db 455 CCAGGCTCTTCCACCAAGACACCTGTGACACAGTTGACATGGCTCCCTCAGCAC 396
OY 634 aggttacccagagctgagagtgctgagctgctgacatcgaacttgcttccagagc 693
Db 395 AGGGTACGAGAGCTGAGAGAGTGTGACGTCGTCATGACTTGTGTGCTTCAGAGAC 336
OY 694 atctccatcaagaagctcgaagcgtctcgaagccctcgaagcccccgaagcgtggt 753
Db 335 AT-TCCATCAAGAGCTCAGAGGCTGCTCAGAGCCCTGAGAGCCCGAGGCTGGGCT 277
OY 754 ccacacccaaggcgagcgagcgtccttgacgtcgaactgacgtcgtcgtcgtcgaag 813
Db 276 CCGACA-CAGGGGGGGGGCGCGGCTTGACAGTGAAGCTGCTGGGGGCTCAGGAG 218
OY 814 ctccgtgagggcgagagagcgagctgctgctgagcgtcgtcgaagcgtcgtgagcc 873
Db 217 CTCTGAGGGGGCGCAGAGAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 158
OY 874 agagatcccgagctgagagagcgctgagagcgcttccctcgtgactgactgact 933
Db 157 AGGATGCCGGGCTGAGAGCGAGCGCTGAGAGCGCTGCTGCTGCTGCTGCTGCTG 98
OY 934 cccctcttatttacttaactcttgagcacccttgacactgacgaagagcttctt 993
Db 97 CCCCCCTATTATTATTCACATCTTGACACCCCTGACCTGAAAGAGGCTTTT 38
OY 994 aaatagaagaatgaggttcttaaa 1019
Db 37 AAATAGAGAAATGAGGTTCTTAA 12

RESULT 12
LOCUS A1857725 445 bp mRNA EST 07-MAR-2000
DEFINITION w121a08.x1 NCI-CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2425526 3',
mRNA sequence.
ACCESSION A1857725
VERSION A1857725.1 GI:5511330
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 445)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R.
Emert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnlnl.gov/bdpr/image/image.html
Insert Length: 1138 Std Error: 0.00
Seq primer: -400p from Gibco
High quality sequence stop: 418.
Location/Qualifiers
1. 445.
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2425526"
/clone_1bp="NCI-CGAP_Ut1"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10b"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1; Salt:
Site_2: Notti; Cloned unidirectionally. Primer: Oligo dt.
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Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
BASE COUNT 100 a 140 c 130 g 75 t
ORIGIN
Query Match 41.3%; Score 445; DB 102; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.9e-82;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 601 tgacacagctgacagctgctccctcctcagacagaggtaccagagctgaagatgtag 660
Db 445 TGCACAGCTGACAGCTGCTCCCTCCTCAGACACAGGCTACAGAGCTGAGAGTGTAG 386
OY 661 cgtgacgcatcagacttggtgcttccagagacatccatcaagaagctcgaagcgtg 720
Db 385 CGTCCCTCATGACATCTGTGTGCTTCCAGAGACATCTCATCAAGAGCTGCAAGGCTG 326
OY 721 ctgcaagccctcgaagcccgagaggtctgaggtcgaacacaaaggcgagccgagcc 780
Db 325 CTGAGAGCCCTGAGAGCCCGAGAGGCTGGGCTCCGACACAAAGGGCGCGCGCGCC 266
OY 781 tgcagctgaagctgctgctcgcgtcagctcagagctcctgagggcgagagcgagctg 840
Db 265 TTGCAGCTGAAAGCTGCTGCTGGGGCTCACAGAGCTCTGCGGGCGCAGAGCGGCTG 206
OY 841 ctggtgagctgctcgtcgaagcgctgagcgctgagccagagatgccgagctgagcgctc 900
Db 205 CTGCTCGGCTGCTGCTGAGAGCGCTGCGCGTGGCCAGCATGCCCGCTGAGCGAGCTC 146
OY 901 cgtgagcgtctcctccctcgtgacgtatccctgagccctcttatttacttaacacctg 960
Db 145 CGTAGAGCGCTTCCTCCTGCTGACATGATCGGCGCCCTCTTATTATCTACATCTTG 86
OY 961 gcaaccactcgaactgaagaagcttctttaaataagaagaatgaggttcttaag 1020
Db 85 GCAACCCACTTGACATGAAAGGGCTTTTAAATAGAAGAAATGAGGTTCTTAAAG 26
OY 1021 ctattttataaagcttttccata 1045
Db 25 CTTATTTTATAAAGCTTTTCATTA 1

RESULT 13
LOCUS BE879166 551 bp mRNA EST 20-OCT-2000
DEFINITION 601486906r1 NIH-MGC_69 Homo sapiens cDNA clone IMAGE:3889296 5',
mRNA sequence.
ACCESSION BE879166
VERSION BE879166.1 GI:10327942
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 551)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnlnl.gov
Plate: L1AM9670 row: 1 column: 01
High quality sequence stop: 546.
Location/Qualifiers
1. 551.
/organism="Homo sapiens"
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: November 2, 2001, 15:03:14 ; Search time 1233.97 Seconds  
(without alignments)  
10153.307 Million cell updates/sec

Title: US-09-006-352-1\_COPY\_115\_924  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues  
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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98: em\_ba3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	810	100.0	1048	89	AF217794	AF217794 Homo sapi
3	810	100.0	1055	10	AX082868	AX082868 Sequence
4	810	100.0	1114	9	AX055373	AX055373 Sequence
5	810	100.0	1114	9	AX056645	AX056645 Sequence
6	810	100.0	1114	88	AF104419	AF104419 Homo sapi
7	810	100.0	1168	9	AX017828	AX017828 Sequence
8	810	100.0	1428	89	AF217793	AF217793 Homo sapi

9	810	100.0	4228	85	AB029011	AB029011 Homo sapi
10	808.4	99.8	5769	93	HS080244	HS080244 Homo sapi
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13	806.8	99.6	936	10	AK098029	AK098029 Sequence
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21	107.2	13.2	1335	10	AX076606	AX076606 Sequence
22	103	12.7	1165	89	AF134187	AF134187 Homo sap
23	103	12.7	1206	10	E15271	E15271 Human mRNA
24	103	12.7	1206	85	AB002146	AB002146 Homo sapi
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VERSION	AF134240.1 GI:4768938
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REFERENCE	Yu,K.Y., Kwon,B., Ni,J., Zhai,Y., Edner,R. and Kwon,B.S. A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses lymfB-mediated apoptosis J Biol Chem. 274 (20), 13753-13756 (1999) 99253915
JOURNAL	2 (bases 1 to 903)
REFERENCE	Kwon,B.S. and Yu,K.Y. Direct Submission Submitted (10-MAR-1999) Micro/Tmunol, Indiana University, 635 Barnhill Drive, Indianapolis, IN 46202, USA location/Qualifiers
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ACCESSION	AF217794
VERSION	AF217794.1 GI:6969262
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ORGANISM	Homo sapiens
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 1048)
JOURNAL	Bal,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X.,
MEDLINE	Sandif,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and
PUBMED	Caskey,C.T.
REFERENCE	Overexpression of M68/DCR3 in human gastrointestinal tract tumors
AUTHORS	Independent of gene amplification and its location in a four-gene
JOURNAL	cluster
FEATURES	Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)
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location	Bal,C.
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Sumneytown Pike, West Point, PA 19403, USA	Location/Qualifiers
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journal	Patent: WO 0110908-A 1 15-FEB-2001;
author	Amgen Inc. (US)
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definition	Sequence 1 from Patent WO0110908.
accession	AX082868
version	AX082868.1 GI:13184802
keywords	human.
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taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
reference	1 (bases 1 to 1055)
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title	Ntr3, a member of the tnfr-receptor supergene family
journal	Patent: WO 0110908-A 1 15-FEB-2001;
author	Amgen Inc. (US)
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LOCUS AX056645  
DEFINITION Sequence 1 from Patent WO0075316.  
ACCESSION AX056645  
VERSION AX056645.1 GI:12309639  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1114)  
AUTHORS Ashkenazi, A.J., Goddard, A., Gurney, A.L., Hillan, K., Napier, M. and Wood, W.I.

TITLE Methods and compositions for inhibiting neoplastic cell growth  
JOURNAL Patent: WO 0075316-A 1 14-DEC-2000;  
Genentech, Inc. (US)  
FEATURES  
source 1. 1114  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 188 a 379 c 356 g 191 t  
ORIGIN

Query Match 100.0%; Score 810; DB 9; Length 1114;  
Best Local Similarity 100.0%; Pred. No. 1.5e-127;  
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 791 GCGTGTGCAAGGCGCTCGAGGCCCCGAGAGGCTGGGCTCGAGACCAAGGCGGCGC 850  
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Db 911 GCGTGTGTTGGGCTGCTGCTGCAAGGCGCTGCGCTGCGCAAGATGCCGGCTTGACCGG 970

Qy 781 agcgtcgttagcgtcttcctcgtgac 810  
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Db 971 AGGCTCGTGAAGCGCTTCTCCCTGTGAC 1000

RESULT 6  
AF104419 1114 bp mRNA PRI 06-JAN-1999  
LOCUS AF104419  
DEFINITION Homo sapiens decoy receptor 3 (DCR3) mRNA, complete cds.  
ACCESSION AF104419  
VERSION AF104419.1 GI:4106877  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1114)  
AUTHORS Pitt, R.M., Marsters, S.A., Lawrence, D.A., Roy, M., Kischkel, F.C., Dowd, P., Huang, A., Donahue, C.J., Sherwood, S.W., Baldwin, D.T., Godowski, P.J., Wood, W.I., Gurney, A.L., Hillan, K.J., Cohen, R.L., Goddard, A.D., Botstein, D. and Ashkenazi, A.  
TITLE Direct Submission  
JOURNAL Submitted (04-NOV-1998) Molecular Oncology, Genentech, 1 DNA Way, San Francisco, CA 94080, USA  
FEATURES  
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Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="20"  
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/note="Linked by radiation-hybrid analysis to chromosome 20 marker AFM218x7"

gene  
CDS

1. 1114  
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/feature="Dcr3"  
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/note="secreted soluble member of the tumor necrosis factor receptor family; amplified in lung and colon cancer."  
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QY 601 cggctcgtcagagccctcgagagcccgagaggtggttcgaacacccaagagcgagcgc 660  
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Db 884 GCGGCTTGCGAGCTGAAGCTGCGCTGCGGCTCAGCGAGCTCCTGGGGGCGCAGAGCGG 943  
QY 721 ggcgtcgtgctgagc 780  
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Db 944 GCGCTGCTGAGGCTGCGGCTGCGAGGCGCTCCTGCGGCTGCGGCTGCGGCTGCGG 1003  
QY 781 agcgctcgtgagc 810  
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Db 1004 AGCGTCGCTGAGGCGCTCCTCCTGTCGAC 1033  
RESULT 8  
AF217793 1428 bp mRNA PRI 12-FEB-2000  
LOCUS Homo sapiens M68C mRNA, alternatively spliced, complete cds.  
DEFINITION AF217793  
ACCESSION AF217793.1 GI:6969260  
VERSION AF217793.1 GI:6969260  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 1428)  
Baï.C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X.,  
Sandig,Y., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and  
Caskey,C.T.  
Overexpression of M68/DCR3 in human gastrointestinal tract tumors  
independent of gene amplification and its location in a four-gene  
cluster.  
Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)  
MEDLINE 20122600  
PUBMED 10655513  
REFERENCE 2 (bases 1 to 1428)  
Baï.C.  
Direct Submission  
Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,  
Summerville Pike, West Point, PA 19403, USA  
JOURNAL  
TITLE Location/Qualifiers  
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SSSSPOCPHNRCTALGALANVPGSSSHDTCTCTGTFPLRVVGAECERAVIDF  
VAFODISIKRLQALALAPGEMGPTPRAGRAALDLKLRRLTELLAGDGLALVRL  
LQALRVARMPGERSYRERFLPVH"  
BASE COUNT 240 a 500 c 448 g 240 t  
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Query Match 100.0%; Score 810; DB 89; Length 1428;  
Best Local Similarity 100.0%; Pred. No. 1.3e-127;  
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 caatgcccccaagacacatttgtcaagcgagcgtgcccgcgagacagcccaagcgtgt 120  
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Db 585 CAGTGGCCCCCAGGCACTTTGTGTACAGGCGCGTGGCCGAGACACCCACAGACGTGT 644  
QY 121 ggcgcgtgtccacacgcgcacatacagcagttcttgaactacttgaagcgtgcgcgtac 180  
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Db 645 GCGCCGTGTCCACCGCGCCACTACACGAGTTTGGAACTACTGGAGCGGTGCGCTAC 704  
QY 181 tgcagcgtctcttgcgagagagcgttgaagagagagcagcgcttgcacgcacacacac 240  
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Db 705 TGCAACTCTCTTCCGGGAGCGGTGAGAGAGAGCAGCGGCTTCCACGCGCACCAAC 764  
QY 241 cgtacccgc 300  
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QY 301 tctgttccacactgtgtgagc 360  
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Db 825 TCGTGTCCACTGCTGCTGCGGCGGTGATGCGCGGCGCACCCGACCAAGACGAGTGC 884  
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QY 601 cggcgtcgtcagagc 660  
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Db 1125 GCGCTGCTGCAAGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1184  
QY 661 ggcgcgttgagcgtgaagc 720  
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Db 1185 GCGGCTTGCAGCTGAAGCTGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCGGCGG 1244  
QY 721 ggcgtcgtgctgagc 780  
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Db 1245 GCGCTGCTGAGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCGG 1304  
QY 781 agcgtcgtgagc 810  
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Db 1305 AGCGTCGCTGAGGCGCTCCTCCTGTCGAC 1334  
RESULT 9  
AB029011 4228 bp mRNA PRI 04-AUG-1999  
LOCUS Homo sapiens mRNA for KIAA1088 protein, partial cds.  
DEFINITION AB029011  
ACCESSION AB029011.1 GI:5689512  
VERSION  
KEYWORDS  
SOURCE Homo sapiens brain cDNA to mRNA, clone\_11b:pluascriptII SK plus  
clone:hk02589.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (sites)  
Kikuno,R., Nagase,T., Ishikawa,K., Hirose,A.M., Miyajima,N.,  
Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.  
Prediction of the coding sequences of unidentified human genes.  
XIV. The complete sequences of 100 new cDNA clones from brain which  
code for large proteins in vitro





QY 601 cggctgtcagagccctcagagcccggaagagctgggggtccagacccaagggcgagcgcc 660  
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Db 775 GCGGCTTGCAAGCTGAAGCTGCGTGGCGGCTCACGAGCTCTCTGGGGCGCAGAGAGCG 834  
QY 721 ggcgcgtgtgtcgcgcgttcagagcgagctgcgttcagagagatcccgagctgagcg 780  
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Db 835 GCGCTGTGTCGCGGCTGTCAGAGCCGTCGCGGTGGCAGATGCCCGGCTCGAGCG 894  
QY 781 agcgtcagagagctccctccctgtgagac 810  
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Db 895 AGCGTCCGTGAGCGCTTCTCCCTGTGTCAC 924

## RESULT 12

AX097545 936 bp DNA PAT 30-MAR-2001  
LOCUS AX097545 Sequence 3 from Patent WO0118055.  
DEFINITION AX097545  
ACCESSION AX097545  
VERSION AX097545.1 GI:13514210  
KEYWORDS  
SOURCE human  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 936)  
Tian, Y. and Wlitcher, D.R.  
TITLE Fluit analog compounds and formulations thereof  
JOURNAL Patent: WO 0118055-A 3 15-MAR-2001;  
ELI LILLY AND COMPANY (US)

## FEATURES

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Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/db\_xref="GI:13514211"

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SSSSSECCOPHRNCTALGALIVGSSSHDTICTSCGFPILSTRVPGARECBRAVIDF  
VARODISIKRLRIOLALEAPGMAPIPRAGRAALQKILRRRTTELLGNQDALLVRL  
LQALRYARMPGLERSVREBFLPVH"

BASE COUNT 132 a 341 c 311 g 152 t  
ORIGIN

Query Match 99.6%; Score 806.8; DB 10; Length 936;  
Best Local Similarity 99.8%; Pred.No. 5; Se-127;  
Matches 808; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 175 CAGTCCCCCGCCAGCAGCTTTGTGACGCGCGCTGCCCGCAGAGAGCCCCACACCTGT 224  
QY 121 ggcgcgtgtccacgcgcgcacacacagcagcttcctgaaactcctgagcgctgcgctac 180  
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Db 235 GCGCGGTGTCACCGCGCCACACGACGAGCTTGTGAACACTCTGAGAGCGCTGCGCTAC 294  
QY 181 tgcacagctcctcgtcgagagcggtgagagagagcagcgcttcgacacgacccacacac 240  
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Db 295 TGCAACGCTCTCTGCGGGAGCGTGAAGAGAGCCACGCGGCTGCCACGCCACCCACAC 354  
QY 241 cgtgccttcgagcgagcgagcttccttcgagcagcgctgttcgttcgtgagacagca 300  
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Db 355 CGTGCTGCGCTGCGGACCGGCTCTTGCCACAGCTGAGTTCGTGTGAGACACAGCA 414  
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QY 301 tctgtccacactgtgtgcgcgctgattgtcccgaggaccccccagacaagcagtg 360  
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Db 415 TCGTGTCCACTGTGTGCGCGGCTGATTGCCCGGAGACCCCGACAGCAACACGAGTGC 474  
QY 361 cagcggtgccccagagacacttcagcagagagctcagctcagctcagctcagctc 420  
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QY 481 accgtgtgacacagctgacagcttcctccctcagacacagaggtacagagagctgagag 540  
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Db 895 AGCGTCCGTGAGCGCTTCTCCCTGTGTCAC 924

## RESULT 13

AX098029 936 bp DNA PAT 30-MAR-2001  
LOCUS AX098029 Sequence 3 from Patent WO0118202.  
DEFINITION AX098029  
ACCESSION AX098029  
VERSION AX098029.1 GI:13514890  
KEYWORDS  
SOURCE human  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 936)  
Tian, Y. and Wlitcher, D.R.  
TITLE Fluit analog compounds and formulations thereof  
JOURNAL Patent: WO 0118202-A 3 15-MAR-2001;  
ELI LILLY AND COMPANY (US)

## FEATURES

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SSSSSECCOPHRNCTALGALIVGSSSHDTICTSCGFPILSTRVPGARECBRAVIDF  
VARODISIKRLRIOLALEAPGMAPIPRAGRAALQKILRRRTTELLGNQDALLVRL  
LQALRYARMPGLERSVREBFLPVH"

BASE COUNT 132 a 341 c 311 g 152 t  
ORIGIN





Em:AW006931 Em:AW272130 Em:AA740147 Em:AA613366  
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RACHATHNARCAKRTGFAGLAFCLAHASCPGAGVAPETPSQNYCCQPCPGTFS  
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Em:AI110378 Em:AW086308 Em:AI952253 Em:AA629904 Em:CO2051  
Em:AI336246 Em:AW204728 Em:AA464125 Em:AI571407  
Em:AI651358 Em:AI969330 Em:AA182473 Em:AI972349  
Em:AI129560 Em:AI073961 Em:165097 Em:AI171678 Em:AA286994  
Em:AA300515 Em:AI968764 Em:R67449 Em:131106 Em:R20968  
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Query Match 47.3% Score 382.8 DB 93 Length 120917;  
Best Local Similarity 79.3% Pred. No. 1, 9e-56;  
Matches 530; Conservative 0; Mismatches 2; Indels 136; Gaps 1;

CDS

1 gcagaaacacccacactaccctctgacgagacgagaaacgagacgagctgtgtgagc 60  
|||||  
455 GCAGAAACACCCACTACCTCTGCGGAGACGCGAGACAGGAGACGCGCTGTGTGCGCC 514  
|||||  
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121 ggcgcgtgtcaccgcgcgacactacacgcagttctggaactactcgtgagcgctgcgtac 180  
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575 GGCCCGTGTCCACCGCGGCACATACACGCACTTGTGGAATCTVAGACCGCTGCCCTAC 634  
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181 tgcacagtcctctgcggggagcgctgagagagagcgacgagcttgcacagcaccacaac 240  
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301 tctgttcacacctgcgtgcgcgctgtatgtgccccg ----- 333  
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Db 755 TCGGTCCACCTGTCGGCCGCGTGAATTCGCCCGGGTGAGAGTGGCGGAGGGAGGGGCC 814  
QY 334 ----- 333  
Db 815 CCCAGAGTGTGGCCGAGAGTGTGGCAGAGGTTCAGATTGCTGTCACACCTTCGACCC 874  
QY 334 -----ggagcccccag 344  
Db 875 TCGAGCTAGACACAGTTCCTCCGACCCGTTCTTCCTCCGTCGTCGACGACCCCCAG 934  
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QY 525 accagag 532  
Db 1115 ACCAGGTG 1122

RESULT 15  
LOCUS AF217796  
DEFINITION Homo sapiens SCG10 like-protein, heliase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRL1) genes, complete cds.  
ACCESSION AF217796  
VERSION AF217796  
KEYWORDS AF217796.1 GI:7012928  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 114793)  
AUTHORS Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X., Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and Caskey,C.T.  
TITLE Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)  
MEDLINE 20122600  
PUBMED 10655513  
REFERENCE 2 (bases 1 to 114793)  
AUTHORS Bai,C., Metzker,M.L., Liu,X. and Caskey,C.T.  
TITLE Direct Submission  
JOURNAL Submitted (20-DEC-1999) WP26A-1000, Merck Research Laboratories, Summeytown Pike, West Point, PA 19403, USA  
FEATURES  
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ORIGIN
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Best Local Similarity 78.9%; Pred. No. 1.3e-55;  
Matches 527; Conservative 0; Mismatches 5; Indels 136; Gaps 1;  
  
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QY     121  ggcgcgtgcacacgcgcacacacagcttcctggaactacctggaagcgtgcgctac 180  
DB 86050  GCGCGGTGTCCACCGCGCCACTACACGAGTTCTGAACTACTGTGAACCTGTGCGGTAC 86109  
QY     181  tgaacgtcctctcgagagagcgltgagagagagacagggcttgcacagccaccacaac 240  
DB 86110  TGCACGTCCTCTCGGGGAGCGTGAAGAGAGGACGCGCTTGCCACGCCACCCACAC 86169  
QY     241  cgtgcctgcgcgtgcgcacagctctcttcgcgcagcgtgttctgtcttggagacgca 300  
DB 86170  CGCGCTTCGCGCTCCGACCGGCTTCTTGCGCACGCGTGTGTTCTGTGGACACGCA 86229  
QY     301  tctgtccacctgtgtcgcgcgtgattgtcccg----- 333  
DB 86230  TCGTGTCCACCTGTGTGCGCGCGCTGATTGCCCGCGGTGAGAGCTGGCGAGGAGGGCC 86289  
QY     334 ----- 333  
DB 86290  CCACAGAGTGTGGCCGAGGTGTGGACGGGTCAAGTTGCTGCTCCAGCCTTGACCC 86349  
QY     334 -----gcaacccccag 344  
DB 86350  TGAGCTAGACACCACTTCCCTGACCTGTCTTCCCTCCGCTGAGGCTGACGCCCCAG 86409  
QY     345  ccaagaacagcagctgagagcgctgcccccaagcaccttccagcagcagctccagctc 404  
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Search completed: November 2, 2001, 15:54:11  
Job time: 3057 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 2, 2001, 13:36:20 ; Search time 76.42 Seconds  
(without alignments)  
6655.330 Million cell updates/sec

Title: US-09-006-352-1\_COPY\_115\_924  
Perfect score: 1 gcagaacaccaccacc.....agcgcttcctcctgtgac 810  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues  
Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Database :

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- 14: /SIDSI/gcgdata/geneseq/geneseqn/NA1993.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	810	100.0	813	20	AAZ25377 Human mFLINT #1 nu
2	810	100.0	813	21	AAA75999 DNA encoding a mat
3	810	100.0	813	21	AAA88730 Human FAS ligand i
4	810	100.0	813	21	AAZ51077 Mature human FLINT
5	810	100.0	900	20	AAZ25375 Human FLINT #1 nuc
6	810	100.0	900	21	AAZ53208 Human Fas ligand i
7	810	100.0	900	21	AAZ51075 Human FLINT coding
8	810	100.0	903	20	AAZ22300 Orphan receptor (H
9	810	100.0	1055	22	AAZ62705 Human NTR3 nucleot
10	810	100.0	1066	21	AAZ53802 M68 TNF receptor r
11	810	100.0	1077	19	AAZ39085 Human tumour necro

12	810	100.0	1077	21	AAA37772 Human tumour necro
13	810	100.0	1114	20	AAZ32744 Human DCR3 polypep
14	810	100.0	1114	21	AAZ58367 Human PRO212 nucle
15	810	100.0	1114	21	AAZ58581 Human PRO212 prote
16	810	100.0	1114	21	AAZ75537 Human PRO212 CDNA
17	810	100.0	1114	22	AAZ84421 Human PRO212 polyp
18	810	100.0	1114	22	AAZ91462 Human PRO212 CDNA
19	810	100.0	1164	19	AAZ07654 Nucleotide sequenc
20	810	100.0	1168	20	AAZ09998 Human lung TNF-rec
21	810	100.0	1205	20	AAZ07226 Human tumour necro
22	810	100.0	1347	21	AAZ63764 Human soluble TNF
23	810	100.0	1428	21	AAZ53801 M68 TNF receptor r
24	810	100.0	1462	20	AAZ76052 Mammalian tumour n
25	808.4	99.8	825	20	AAZ25378 Human mFLINT #2 nu
26	808.4	99.8	825	21	AAZ51078 Human mature FLINT
27	808.4	99.8	936	20	AAZ25376 Human FLINT #2 nuc
28	806.8	99.6	936	21	AAZ88731 Human FAS ligand i
29	806.8	99.6	936	21	AAZ51076 Human FLINT coding
30	806.8	99.6	936	22	AAZ7696 Human FLINT native
31	806.8	99.6	1137	21	AAZ92404 CDNA encoding huma
32	727.4	89.8	900	21	AAZ53209 Monkey Fas ligand
33	727.4	89.8	900	21	AAZ53209 Monkey Fas ligand
34	641.2	79.2	767	20	AAZ3419 Human APO6 DNA. H
35	530.4	65.5	1859	21	AAZ63765 Human soluble TNF
36	473.4	58.4	491	20	AAZ32745 Human DCR3 EST seq
37	459	56.7	459	21	AAZ84621 Human TNFR superfa
38	459	56.7	459	20	AAZ63757 Human TNFR soluble
39	394.4	48.7	397	20	AAZ07227 Human tumour necro
40	384.4	47.5	1667	19	AAZ39086 Human tumour necro
41	384.4	47.5	1667	21	AAZ37773 Human tumour necro
42	378	46.7	7720	21	AAZ53800 Genomic DNA encod1
43	245.2	30.3	271	20	AAZ32747 Human DCR3 EST seq
44	242.2	29.9	283	20	AAZ32752 Human DCR3 EST seq
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# ALIGNMENTS

RESULT 1	
ID	AAZ25377 standard; cDNA: 813 BP.
AC	AAZ25377;
XX	
DT	17-DEC-1999 (first entry)
XX	
DE	Human mFLINT #1 nucleotide sequence.
XX	
KW	Human: mFLINT; OP03; tumour necrosis factor receptor; FasL;
KW	apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW	sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW	reperfusion associated injury; aplastic anaemia; differentiation;
KW	growth; myelodysplastic syndrome; pancytopenic condition;
KW	myocardial ischaemia; ss.
XX	
OS	Homo sapiens.
XX	
PN	W09550413-A2.
PD	07-OCT-1999.
XX	
PF	30-MAR-1999; 99WO-0506797.
XX	
PR	30-MAR-1998; 98US-0079856.
PR	20-MAY-1998; 98US-0086074.
PR	09-SEP-1998; 98US-0099643.
PR	17-DEC-1998; 98US-0112577.
PR	18-DEC-1998; 98US-0112703.
PR	18-DEC-1998; 98US-0112933.
PR	22-DEC-1998; 98US-0113407.
XX	
PA	(FLIL ) LILLY & CO ELL.

XX Bumlol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;  
PI Hui KY, Kharitonov A, Mizrahi J, Na S, Nodlitt TW, Reidy CA;  
PI Song HY, Wang J, Wu X, Zuckerman SH;  
XX  
DR WPI: 1999-591319/50.  
DR P-PSDB: AA42184.  
XX  
XX  
PT Use of mature F1NF for treating acute liver failure, inflammation,  
PT cancer, and diabetes by prevention of FasL-Fas mediated apoptotic  
PT and proinflammatory activity  
XX  
XX Claim 29; Fig 3; 9pp; English.

CC The present invention describes therapeutic applications of mature FLINT  
CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT  
CC (mFLINT), which is a member of the tumour necrosis factor receptor  
CC superfamily, is used for treating acute liver failure, inflammation of  
CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated  
CC with inflammation, hepatitis, abnormal apoptosis, an ischemia-associated  
CC injury or disorder such as hypercoagulation (including use with  
CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury  
CC or disorder, Type I diabetes, cancer cell damage or damage to an  
CC innocent bystander tissue that is induced by a chemotherapeutic agent or  
CC therapeutic irradiation, treating hematopoietic progenitor cells that  
CC have been exposed to therapeutic radiation or chemotherapy, aplastic  
CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is  
CC also used for promoting the growth or differentiation of a hematopoietic  
CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte  
CC resulting from abnormal myocardial ischemia. The present sequence  
CC encodes human mFLINT.

XX  
XX Sequence 813 BP, 122 A, 298 C, 267 G, 126 T, 0 other;

Query Match	100.0%	Score 810;	DB 20;	Length 813;
Best Local Similarity	100.0%	Pred. No. 5.9e-145;		
Matches 810; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

[illegible][illegible]

## RESULT

ID AAA75999 standard; DNA; 813 BP.

AC AAA75999;

DT 19-FEB-2001 (first entry)

DE DNA encoding a mature human FAS Ligand Inhibitory Protein (FLINT).

KW Human; FAS Ligand Inhibitory protein; FLINT; analogue; apoptosis; tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis

acute respiratory distress syndrome; ulcerative colitis; chronic obstructive pulmonary disease; Crohn's disease; kw

XX  
XX  
Homo sapiens

AA  
PN  
W0200058465-

05-OCT-2000  
PD  
AA

20-MAR-2000; 2000WO-US06417.

PR 30-MAR-1999; 99US-0126839.

PR 21-JUN-1999; 99US-0140156.

PR 18-FEB-2000; 2000US-0183398.

PA (ELL) LILLY &amp; CO ELL

PI Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;

PI Wroblewski VJ;

DR WPI: 2000-656167/63

[illegible]

PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis, chronic obstructive pulmonary disease, emphysema, cystic fibrosis or CrebA's

pt disease - .

ps claim 3/; Page 113; 114pp; English.

CC The present sequence encodes a mature human FAS ligand inhibitory  
CC protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor  
CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature  
CC FLINT protein is modified to produce analogues, which have greater  
CC potency, longer in vivo half-lives, decreased aggregation, decreased

CC absorption onto surfaces, increased solubility and improved ease of  
CC formulation. The FLINT analogue is useful for treating a patient  
CC suffering from disease or condition relating to abnormal apoptosis such  
CC as acute lung injury, acute respiratory distress syndrome, pulmonary  
CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or  
CC Crohn's disease.

XX Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;  
SQ

Query Match	100.0%	Score 810;	DB 21	Length 813;
Best Local Similarly	100.0%;	Pred. No. 5.9e-145;		
Matches 810; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

[illegible]

RESULT 3  
AAA88730

1D	AA88730 standard; cDNA; 813 BP.
XX	
AC	AA88730;
XX	
DT	05-FEB-2001 (first entry)
XX	
DE	Human FAS ligand inhibitor protein FLINT cDNA.
XX	
KW	FLINT; FAS ligand inhibitor protein; human; protease resistant;
KW	acute lung injury; acute respiratory distress syndrome;
KW	chronic obstructive pulmonary disease; pulmonary fibrosis;
KW	ulcerative colitis; therapy: organ transplantation; ss.
XX	
OS	Homo sapiens.
XX	
PN	W0200058466-A2.
XX	
PD	05-OCT-2000.
XX	
PF	20-MAR-2000; 2000WO-US06418.
XX	
PR	30-MAR-1999; 99US-0126839.
PR	21-JUN-1999; 99US-0140073.
PR	04-AUG-1999; 99US-0147071.
PR	20-OCT-1999; 99US-0160524.
PR	21-OCT-1999; 99US-0160669.
PR	20-DEC-1999; 99US-0172744.
PR	26-JAN-2000; 2000US-0178184.
XX	
PA	(ELIL ) LILLY & CO ELI.
XX	
PI	Micanovic R, Rathnachalam R, Wltcher DR;
XX	
DR	WPI: 2000-664925/64.
XX	
DR	P-PSDB; AAB19705.
XX	
PT	Novel protease resistant FAS ligand inhibitor protein analogues
PT	resistant to in vivo or in vitro proteolysis at amino acid position 218
PT	of the mature protein, useful for treating autoimmune diseases
XX	
PS	Disclosure; Page 95; 100pp; English.
XX	
CC	The present sequence is that of cDNA coding for human FAS ligand
CC	inhibitory protein FLINT mature protein (see AAB19705). FLINT is a
CC	tumour necrosis factor receptor homologue that binds FAS ligand,
CC	preventing its interaction with FAS. This interaction is implicated
CC	in runaway apoptosis and inflammatory disease. FLINT also binds to
CC	LIGHT, a membrane-bound ligand, which may play a role in immune
CC	modulation and apoptosis. The invention relates to novel FLINT
CC	analogues (see also AAB19706-09) that are resistant to proteolysis
CC	by trypsin-like proteases between positions 218 and 219 of the
CC	FLINT mature protein sequence. Nucleic acids, vectors and
CC	transformed host cells for recombinant production of the analogues
CC	are claimed. FLINT cDNA is used as a template for introducing the
CC	required point mutations e.g. via PCR mutagenesis. The protease
CC	resistant FLINT analogues are used to prevent or treat acute lung
CC	injury, acute respiratory stress syndrome, ulcerative colitis,
CC	chronic obstructive pulmonary disease, pulmonary fibrosis, to
CC	inhibit T lymphocyte activation, and to facilitate organ
CC	preservation for transplantation (claimed).
XX	
XX	Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Query Match	100.0%	Score 810;	DB 21;	Length 813;
Best Local Similarly	100.0%;	Pred. No. 5,9e-145;		
Matches 810; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

61 cagtcgccccccagcgacacttctgttcagcggcgccgacgacgagacagccccaacacgtct 120  
 0y 1 gcaagaagaacccacttaccctctgcgggacgcgaagaagcaggcggtggtgtgtgccc 60  
 Db 4 gcaagaagaacccacttaccctctgcgggacgcgaagaagcaggcggtggtgtgtgccc 63

[illegible][illegible]



QY	421	caagcaacatgcaagagcccgaggcgctgagccctcaatgctgcaagagctctctccatgac	480
Db	424	caaccgcaacatgcaagagcccgaggcgctgagccctcaatgctgcaagagctctctccatgac	483
QY	481	acccttgacacacagctgacatctgctctccctcacaagcaacagaggctacagagatctgagag	540
Db	484	acccttgacacacagctgacatctgctctccctcacaagcaacagaggctacagagatctgagag	543
QY	541	tgtgaaagctgacgctcatalcgaactgtgagctctccagaagacatctccatcaaaagagctgacag	600
Db	544	tgtgaaagctgacgctcatalcgaactgtgagctctccagaagacatctccatcaaaagagctgacag	603
QY	601	cggctgctgctcagagccctccagagagcccgaaagagctgaggtctccagacacaaagagcgagcgac	660
Db	604	cggctgctgctcagagccctccagagagcccgaaagagctgaggtctccagacacaaagagcgagcgac	663
QY	661	gcgagccctgacagatcgaagagctgctgcagcgctcacagagatctccctgagagcgagacagag	720
Db	664	gcgagccctgacagatcgaagagctgctgcagcgctcacagagatctccctgagagcgagacagag	723
QY	721	gcgagctgctgctgctgagcgctgctgacagagcgctgctgcagctgagccagagatctccagagcgag	780
Db	724	gcgagctgctgctgctgagcgctgctgacagagcgctgctgcagctgagccagagatctccagagcgag	783
QY	781	agcgctccgctgagcgctctccctccctgctgac	810
Db	784	agcgctccgctgagcgctctccctccctgctgac	813

RESULT	5	
AA225375		
ID	AA225375	standard; cDNA; 900 BP.
XX		
AC	AA225375;	
XX		
DT	17-DEC-1999	(first entry)
XX		
DE	Human FLINT #1 nucleotide sequence.	
XX		
KW	Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;	
KW	apoptosis; inflammation; cancer; diabetes; acute liver failure;	
KW	sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;	
KW	repertusion-associated injury; aplastic anaemia; differentiation;	
KW	growth; myelodysplastic syndrome; pancytopenic condition;	
KW	myocardial ischaemia; ss.	
OS	Homo sapiens.	
XX		
PN	W09950413-A2.	
PD	07-OCT-1999.	
XX		
PE	30-MAR-1999; 99MO-US06797.	
XX		
PR	30-MAR-1998; 98US-0079856.	
PR	20-MAY-1998; 98US-0086074.	
PR	09-SEP-1998; 98US-0099643.	
PR	17-DEC-1998; 98US-0112577.	
PR	18-DEC-1998; 98US-0112703.	
PR	18-DEC-1998; 98US-0112933.	
PR	22-DEC-1998; 98US-0113407.	
XX		
PA	(ELIL ) LILLY & CO ELI.	
XX		
PI	Bumol TF, Dou S, Glasbrook AL, Gould KE, Hale JE, Heuer JG;	
PI	Hui KJ, Kharitonovkov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;	
PI	Song HY, Wang J, Wu X, Zuckerman SH;	
XX		
DR	WPI: 1999-591339/50.	
XX		
PT	P-PSDB; AAY42182.	
XX		

Use of mature FLINT for treating acute liver failure, inflammation, cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic

PT	and proinflammatory activity
XX	
PS	Claim 28; Fig 1; 99pp; English.

The present invention describes therapeutic applications of mature FLINT (mFLINT) for use in the treatment of acute liver failure. Mature FLINT (mFLINT), which is a member of the tumour necrosis factor receptor superfamily, is used for treating acute liver failure, inflammation of the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated injury or disorder such as hypercoagulation (including use with thrombolytic or anti-thrombolytic agents), reperfusion-associated injury or disorder, type I diabetes, cancer, cell damage or damage to an innocent bystander tissue that is induced by a chemotherapeutic agent or therapeutic irradiation, treating haematopoietic progenitor cells that have been exposed to therapeutic radiation or chemotherapy, aplastic anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is also used for promoting the growth or differentiation of a haematopoietic progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte resulting from abnormal myocardial ischaemia. The present sequence encodes human FLINT.

Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;

Query Match	100.0%	Score 810;	DB 20;	Length 900;
Best Local Similarity	100.0%;	Pred. No. 6e-145;		
Matches 810; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]



XX	AAA51075:
AC	
XX	
DT	26-SEP-2000 (first entry)
XX	
DE	Human FLINT coding sequence.
XX	
KW	FLINT: osteoprotegerin 3; OPG3: tumour necrosis factor receptor; TNFR;
KW	FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW	anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
KW	anti-inflammatory; antibacterial; immunosuppressive; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	CDS
FT	1..900
FT	/tag= a
FT	/product= FLINT
FT	/partial
FT	1..87
FT	sig-peptide
FT	/tag= b
FT	mat-peptide
FT	88..900
FT	/tag= c
PN	MO200037094-A2.
XX	
PD	29-JUN-2000.
XX	
PF	21-DEC-1999: 99WO-US30734.
PR	
PR	22-DEC-1998: 98US-O113407.
PR	30-MAR-1999: 99WO-US06797.
PR	20-OCT-1999: 99US-O172239.
XX	
XX	(ELIL ) LILLY & CO ELI.
PI	
PI	Cohen FJ, Posada JA, Wierda D;
DR	WPI; 2000-475441/41.
DR	P-PSDB; AAY96596.
PT	
PT	Use of mature FLINT for treating e.g. acute respiratory distress
PT	syndrome, ulcerative colitis or ischemic injury during organ
PT	transplantation
PS	
PS	Example 7: Fig 1A-B; 125pp; English.
XX	
XX	Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis
XX	factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
XX	mediates FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
XX	induced apoptotic and pro-inflammatory activity. mFLINT is useful for
XX	treating acute respiratory distress syndrome, treating or inhibiting
XX	ulcerative colitis, inhibiting ischemic injury during organ
XX	transplantation or for organ preservation during transplantation. mFLINT
XX	can also be used to treat acute liver failure, inflammation of the liver,
XX	abnormal (hepatocyle) apoptosis, sepsis, disorders associated with
XX	inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
XX	damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
XX	type I diabetes, cancer, damage to an innocent bystander tissue induced
XX	by a chemotherapeutic or therapeutic irradiation aplastic anaemias,
XX	myelodysplastic syndromes and pancytopenic conditions.
XX	
XX	Sequence 900 BP; 128 A; 324 C; 304G; 144 T; 0 other;

	Query Match	100.0%	Score 810;	DB 21;	Length 900;	
	Best Local Similarity	100.0%	Pred. No. 6e-145;			
	Matches 810; Conservative	0;	Mismatches	0;	Indels	0;
Oy	1	gcagaacaaccacattacctgtgctggagcgcagagagacagaggcgagctgtgttgcgcc	60			
Db	91	gcagaacaaccacattacctgtgctggagcgcagagagacagaggcgagctgtgttgcgcc	150			

[illegible]

RESULT	8
AAK22300	
ID	AAK22300 standard; DNA; 903 BP.
XX	
AC	AAK22300;
XX	
DT	20-MAY-1999 (first entry)
XX	
DE	Orphan receptor (HUMAN NTR-1) polypeptide encoding DNA.
XX	
KW	HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;
KW	tumour necrosis factor receptor; muscle disorder; bone mass; screening
KW	muscle metabolism; binding agent; cognate ligand; ss.
XX	
OS	Homo sapiens.
XX	
PN	W09907738-A2.
XX	
XX	18-FEB-1999.
PD	
XX	

PF 04-AUG-1998: 98WO-US16202.  
XX  
PR 06-AUG-1997: 97US-0054869.  
XX  
PA (PROC ) PROCTER & GAMBLE CO.  
XX (REGE-) REGENERON PHARM INC.  
XX  
PI Maslakowski PJ, Morris J, Valenzuela DM;  
DR WPI: 1999-167365/14.  
DR P-PDB: AAM95082.  
XX  
PT Novel orphan human receptor polypeptide and nucleic acid - useful as  
XX diagnostic reagents and for treatment of muscle disorders  
XX  
PS Claim 2: Page 21: 23pp: English.  
XX  
CC This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The  
XX protein is related to osteoprotegerin (OPG) and to tumour necrosis factor  
XX receptor (TNFR). Host cells transformed with a vector comprising the  
XX HUMAN NTR-1 nucleic acid are used for the recombinant expression of the  
XX protein. HUMAN NTR-1 proteins and antibodies immuno specific for the  
XX protein are useful for diagnosis and treatment of humans and animals,  
XX especially muscle disorders, as the receptor is involved in regulation  
XX of bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful  
XX for screening for novel binding agents, and cognate ligands, which may be  
XX used to treat disorders associated with HUMAN NTR-1 imbalance.  
XX  
XX Sequence 903 BP; 129 A; 324 C; 305 G; 145 T; 0 other;

[illegible]

RESULT	9
AAFG2705	
ID	AAFG2705 standard; cDNA; 1055 BP
XX	
AC	AAFG2705;
DT	02-MAY-2001 (first entry)
XX	
DE	Human NTR3 nucleotide sequence.

KM Human: R3: tumour necrosis factor receptor; TNF receptor; anti-HIV;  
KM antianaemic; immunosuppressive; antidiabetic; antiviral; antibacterial;  
KM cytostatic; neuroprotective; antinflammatory; anorectic; vasotropic;  
KM antihemorrhagic; cerebroprotective; antitubercular; tuberculostatic;  
KM gene therapy; cancer; blood disorder; brain disorder; autoimmune disease;

XX		
OS	Homo sapiens.	
XS		
PN	MO200110908-A1.	
XX		
PD	15-FEB-2001.	
XX		
PF	02-AUG-2000; 2000OWO-US21287	
XR		
04-AUG-1999;	99US-0147297	

PA (AMGE-) AMGEN INC.  
XX PI  
XX Hsu H;  
XX  
DR WPI: 2001-191521/19  
P-PSDB; AAB71754.  
DR

PT New tumor necrosis factor receptor, NTR3, useful for treating cancers  
 PT stroke, anemia, obesity, Rheumatoid arthritis and transplantation  
 PT rejection - 155pp; English.  
 XX  
 XX Claim 1; Page 128-129; 135pp; English.

The present sequence encodes the tumour necrosis factor (TNF) receptor polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful for treating diseases such as acquired-immunodeficiency syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria, diabetes mellitus, disseminated intravascular coagulopathy, erythroid sick syndrome, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia, obesity, rejection of transplanted organs, rheumatoid arthritis, septic shock syndrome, stroke, adult respiratory distress syndrome (ARDS), tuberculosis, and a number of viral diseases. The NTR3 polypeptide is useful for identifying or developing new (anti)agonists of NTR3. It may be used as an immunogen to which antibodies may be raised. NTR3 nucleic acid molecules may be useful as hybridisation probes in diagnostic assays to test, either qualitatively or quantitatively, for the presence of an



Matches	810;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

Oy	1	g g g a a a c c c c c c t a c c c c t g g c g g a g a c a g a a a c a g g g a g a g c g t g t t g c g c	60
Dp	143	g c a a a a c a c c c c c t a c c c c t g g g a g a c a g a g a g g a g c g t g t t g c g c	2020
Oy	61	c a a t g c c c c c a g a g c a c c t t t g t c a g c g c g t g c c g a a a a g c c c a a g a c t g t	1220
Dp	203	c a g t g c c c c c a g a c a c t t t g t c a g c g c g t g c c g a a a a g a c a g c c a a g a c t g t	2626
Oy	121	g g c c c g t t g c a c a c g c g c a c a t a a c g a a t t c t g a a c t a c t c t g a g c g t g c g a t a c	1808
Dp	263	g g c c c g t t g c a c a c g c g c a c a t a a c g a g t t c t g a a c t a c t c t g a g c g t g c g a t a c	3222
Oy	181	t g a a a g t c t c t t g g g g a a c t g a g a g a g a g a c a c g g t t t g a c a a g c a c c a a a c	2404
Dp	323	t g a a a g t c t c t c t g g g a g a c t g a g a g a g a g a g a c a c g g t t t g a c a a g c a c c a a c	3026
Oy	241	c g t g c t g c c g c t g c g a c a c a c g g c t t t c t t g c a a c g c t g t t c t g c t t g a g a c g c a	3000
Dp	383	c g t g c t g c c g c t g c g a c a c a c g g c t t c t t g c a a c g c t g t t c t g c t t g a g a c g c a	4422
Oy	301	t c g t g t c c a c t g t g t g c g g g t g a t t g c c c c g g g a c c c c c a g c c a a a c a c a c g a t g c	3606
Dp	443	t c g t g t c c a c a c t g g t g c g g g a g t a t t g c c c c g g g a c c c c c a g c c a a a c a c g a t g c	5020
Oy	361	c a g c g c g t g c c c c c a g a g c a c c t t c t c a g a c a g c a g c t c c a g t c a g a g a g t g c a g c c	4202
Dp	503	c a g c g c g t g c c c c c a g a g c a c c t t c t c a g a c a g c a g c t c c a g a g a g a g t g c a g c c	5622
Oy	421	c a c c g c a a c t g c a c g a g c c c t g g g c c t c a a t g t g c a g a g c t c t c t c c c a t g a c	4804
Dp	563	c a c c g c a a c t g c a c g a g c c c t g g g c c t c a a t g t g c a g a g c t c t c t c c c a t g a c	6222
Oy	481	a c c c t g t g c a c c a g c t g c a c t g a g c t t c c c c c t a g a c a c a a g g t a c c a g a g c t g a g a g	5404
Dp	623	a c c c t g t g c a c c a g c t g c a c t g a g c t t c c c c c t a g a c a c a a g g t a c c a g a g c t g a g a g	6026
Oy	541	t g t g a g a g t g c g a t c a c t g a c t t t g t g c t t c c a a g a a c a t c a t c a t a a a a g a g c t g a g	6000
Dp	683	t g t g a g a g t g c g a t c a c t g a c t t t g t g c t t c c a a g a a c a t c a t c a t a a a a g a g c t g a g	7422
Oy	601	c g g c t g c a g a g c c c t c g a a g a c c c c g a a g a g c t g a g g t c t c a a c a c c a a a g g c g g c g c	6606
Dp	743	c g g c t g c a g a g c c c t c g a a g a c c c c g a a g a g c t g a g g t c t c a a c a c c a a a g g c g g c g c	8020
Oy	661	g c g g c c t t g c a a c t g a a a g c t g c t c g a c g g c t c a c a g a g a c c c t c t g g g g c g a a g a c g g	7202
Dp	803	g c g g c c t t g c a a c t g a a a g c t g c t c g a c g g c t c a c a g a g a c c c t c t g g g g c g a a g a c g g	8826
Oy	721	g c a c t g a c t g a c a g c t g c t g c a a g a g c t g a c g t g c a a g a t a t g c c c g g g c t g a a c g g	7804
Dp	863	g c a c t g a c t g a c a g c t g c t g c a a g a g c t g a c g t g c a a g a t a t g c c c g g g c t g a a c g g	9222
Oy	781	a g c t c g a t g a a g a g c t t c c t c c c t g a c	810
Dp	923	a g c t c g a t g a a g a g c t t c c t c c c t g a c	952

RESULT: 11	
AAV39085	
ID	AAV39085 standard; CDNA; 1077 BP.
XX	
XX	
XX	AAV39085;
XX	
DT	26-OCT-1998 (first entry)
XX	
DE	Human tumour necrosis factor receptor-6 alpha CDNA.
XX	
KW	Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta; endoethelial cells; keratinocytes; normal prostate; apoptosis; prostate tumour tissue; ss.
KW	

OS	Homo sapiens.	
XX		
FH	key	location/Qualifiers
Ft	CD5	25..927
Ft		/*tag= a
Ft	sig_peptide	/product= "TWFR-6 alpha protein"
Ft		25..114
Ft		/*tag= b
Ft	mat_peptide	115..924
Ft		/*tag= c

PN WO9830694-A2.  
 XX 16-JUL-1998.  
 PD 13-JAN-1998;  
 XX 98WO-US00153.  
 PF 14-JAN-1997;  
 XX 97US-0035496.  
 PR 14-JAN-1997;  
 XX 97US-0035496.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX  
 PI Edner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;  
 XX WPI: 1998-399142/34.  
 DR P-PsDB: AAM63622.  
 XX  
 XX  
 PT human tumour necrosis factor receptors 6-alpha and 6-beta - used in  
 PR the diagnosis of immune system-related disorder(s)  
 XX  
 XX Disclosure: Flg 1: 91pp: English.

CC The present sequence represents the human tumour necrosis factor  
CC receptor-6 alpha (TNFR-6 alpha) cDNA. The invention also provides  
CC for the TNFR-6 beta cDNA (AA133086). TNFR-6 alpha and TNFR-6 beta are  
CC members of the tumour necrosis factor receptor (TNFR) family. TNFRs  
CC are expressed in endothelial cells, keratinocytes, normal prostate and  
CC prostate tumour tissue. For a number of disorders of these cells,  
CC particularly of the immune system, substantially altered (whether  
CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta  
CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6  
CC polypeptides, nucleic acids and antibodies are claimed to be useful in  
CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and  
CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are  
CC also claimed to be useful for identifying ligands which may be useful  
CC in the treatment of apoptosis related disorders.

XX Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;

Query Match	100.0%	Score 810	DB 19	Length 1077
Best Local Similarity	100.0%	Pred. No. 6e-145		
Matches 810	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	gagagaaacaccacactaccctctgagcgagacgagagagagagcgctgtgtgccc	60	
Dh	115	ggcgaaacaccaccactcccctggcgagagcgagagagagagagcgctgtgtgccc	174	
Qy	61	cgatgcgcccccaggagaccttltgtgacgcgcgctgtgccgagacagcccagacgtgt	120	
Dh	175	cgatgcgcccccaggagacacttltgtgacgcgcgctgtgccgagacagcccagacgtgt	234	
Qy	121	gagccctgttcacacgcgcgcactacacagcagttcttgagacactcttgagacgcctgcgcgtac	180	
Dh	235	ggccctgtgtccacacgcgcgcactacacagcagttcttgagacactcttgagacgcctgcgcgtac	294	
Qy	181	tgcacagctccctctcgcggagagcgttgagagagagacagggcctgtgcacgcgcccccacac	240	
Dh	295	tgcacagctccctctcgcggagagcgttgagagagagacagggcctgtgcacgcgcccccacac	354	
Qy	241	cgtgcctcgcgcctcgcacacgcgctctctcgcgcacgcctgtgtcttcgcctgtgagacga	300	
Dh	355	cgtgcctcgcgcctcgcacacgcgctctctcgcgcacgcctgtgtcttcgcctgtgagacga	414	









XX DE Human PRO212 protein UNQ186 encoding cDNA SEQ ID NO:13.  
XX  
KW Human; immune related disease; diagnosis; anti-inflammatory; cardiant;  
KW dermatological; antarthritic; antirheumatic; immunosuppressive;  
KW haemostatic; antithyroid; antidiabetic; nocotropic; neuroprotective;  
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
KW osteoarthritis; systemic lupus erythematosus; rheumatoid arthritis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopenia; immune-mediated renal disease;  
KW demyelinating disease; hepatobiliary disease; diabetes mellitus;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW immunological disease; immune-mediated skin disease; allergic disease;  
KW graft rejection; graft-versus-host-disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200053758-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 02-MAR-2000; 2000WO-US05841.  
XX  
PR 08-MAR-1999; 99WO-US050528.  
PR 10-MAR-1999; 99US-0123618.  
PR 12-MAR-1999; 99US-0123957.  
PR 23-MAR-1999; 99US-0125775.  
PR 12-APR-1999; 99US-0128849.  
PR 20-APR-1999; 99WO-US08615.  
PR 28-APR-1999; 99US-0131445.  
PR 04-MAY-1999; 99US-0132371.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-OCT-1999; 99US-0162506.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28531.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 16-DEC-1999; 99WO-US28565.  
PR 20-DEC-1999; 99WO-US30095.  
PR 30-DEC-1999; 99WO-US31774.  
PR 03-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AU, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
PI Kabackoff RC, Lu Y, Pan J, Pennica  
PI Stewart TA, Tumas D, Matanabe CK, Wood WI, Yan M;  
XX  
DR WPI, 2000-572271/53.

DR P-Psdb; AAB33416.  
XX  
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus  
XX  
XX  
PS Claim 23; Fig 5; 309pp; English.  
XX  
CC The present invention describes sixty four human PRO proteins which can  
CC be used in the treatment of immune related diseases. The human PRO  
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
CC treating and diagnosing immune related disorders. The disorders are  
CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease.  
CC Autoimmune or immune-mediated skin diseases, allergic diseases,  
CC immunological diseases of the lung, and transplantation associated  
CC diseases including graft rejection and graft-versus-host-disease.  
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 1114 BP; 188 A; 379 C; 356 G; 191 T; 0 other;  
  
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Best local similarity 100.0%; Pred. NO. 6e-145;  
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 191 gcgaagaacccaccctacccttgaggagagcagcagagagagcagctgtgtgccc 250  
  
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Db 251 cagtgccccccagagaccttggcagcgcgtgcccgcagagagagccagcagctgt 310  
  
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Db 431 cgtgtcctgcgcgtgcgcacgcgcttcttcgcgcagcgtgtgttctgttggagacgca 490  
  
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QY 361 cagcgcgtgccccccagagaccttccagccagcagagctccagctcagagcagtgccagccc 420  
Db 551 cagcgcgtgccccccagagaccttccagccagcagagctccagctcagagcagtgccagccc 610  
  
QY 421 cagcgcagactgcagcgccttggtgcctcctcaagtgcagggcttctccccaagac 480  
Db 611 cagcgcagactgcagcgccttggtgcctcctcaagtgcagggcttctccccaagac 670  
  
QY 481 acccgtgcacagctgcagtggtctcccccctcagcagcagaggtacagggagctggaag 540  
Db 671 acccgtgcacagctgcagtggtctcccccctcagcagcagaggtacagggagctggaag 730  
  
QY 541 tctgagcgtgcgcgtcagctgtgtgcttccagggagatcatcaagaagctgcag 600

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Search completed: November 2, 2001, 15:05:24  
Job time: 5344 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 30, 2001, 14:44:00 ; Search time 1010.9 Seconds  
(without alignments)  
7574.252 Million cell updates/sec

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Perfect score: 810  
Sequence: 1 gcagaaacaccaccacc.....agcgctccctccctgtgcac 810

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 segs, 4726426750 residues  
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	577	71.2	679	141 BE878006	BE878006 601489784
3	496.8	61.3	874	147 BF339551	BF339551 602039016
4	482.6	59.6	692	111 AM083241	AM083241 xc07a04.x
5	466.8	57.6	600	113 AM262121	AM262121 xc31d04.x
6	421.6	52.0	551	114 BE879166	BE879166 601486906
7	411.6	50.8	540	116 AM471440	AM471440 xc59e06.x
8	388	47.9	554	116 AM464298	AM464298 BP230015A
9	387.2	47.8	514	119 AM662363	AM662363 h125f01.x
10	381.4	47.1	475	24 AT1718743	AT1718743 as95h04.x
11	374	46.2	697	141 BE873766	BE873766 601483915
12	359	44.3	478	143 BF001490	BF001490 7988h10.x
13	354	43.7	515	111 AM083914	AM083914 xc25902.x
14	345.2	42.6	459	110 AM014771	AM014771 UI-H-B10-
15	324	40.0	445	110 AT1857725	AT1857725 w121a08.x
16	311.8	38.5	453	113 AM204999	AM204999 UI-H-B11-
17	308.8	38.1	467	1 AA025673	AA025673 z99h09.s
18	308	38.0	436	18 AT290210	AT290210 q179912.x
19	305	37.7	452	120 AM771720	AM771720 h171a02.x
20	300	37.0	430	22 AT1561219	AT1561219 tq27c11.x
21	286	35.3	468	120 AM769220	AM769220 h154h07.x
22	282.4	34.9	340	114 AM316995	AM316995 x10e06.x
23	281.8	34.8	417	110 AM006931	AM006931 wt08b06.x
24	280	34.6	405	21 AT520716	AT520716 tl06f10.x
25	279	34.4	359	111 AM080544	AM080544 xc33a03.x
26	271.2	33.5	295	120 AM801019	AM801019 MR3-DM006
27	267.4	33.0	388	151 BF591174	BF591174 7h54h12.x
28	260.6	32.2	428	3 AA155701	AA155701 z070e05.x
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31	250.2	30.9	344	17 AT1185297	AT1185297 qe36c02.s
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33	239.4	29.6	461	11 AA740147	AA740147 ob26a08.s
34	237	29.3	358	18 AT182851	AT182851 qt84e09.x
35	227.4	28.1	378	9 AA613366	AA613366 nq31a08.s
36	218.6	27.0	423	111 AM083605	AM083605 xc19h07.x
37	198	24.4	333	122 AM955349	AM955349 EST367419
38	195	24.1	211	102 AT1862475	AT1862475 td16h06.x
39	183	22.6	233	1 AA025672	AA025672 z99h09.r
40	181	22.3	378	19 AT180034	AT180034 tq19e10.x
41	179	22.1	191	5 AA325843	AA325843 EST28933
42	178	22.0	271	141 BE871829	BE871829 601489305
43	166.2	20.5	413	114 AM272130	AM272130 xul0h06.x
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## ALIGNMENTS

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DEFINITION	BE878908	mRNA sequence.				
ACCESSION	BE878908	GI:10327684				
VERSION	BE878908.1					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homindae; Homo.					
TITLE	NIH-MGC http://mgi.nci.nih.gov/					
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)					
COMMENT	Unpublished (1999)					
CONTACT	Robert Strausberg, Ph.D.					

Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTF/gazdar  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM9685 row: a column: 03  
High quality sequence stop: 617.  
Location/Qualifiers

## FEATURES

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/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lung; Vector: pCMV-Sp0R6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
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BASE COUNT  
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ORIGIN

Query Match 73.3%; Score 594; DB 141; Length 617;  
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3 CTGGAACCTACTGAGCGCTGCCGCTACTGCAACGCTCTGCGGGAGCGTAGAGA 62  
213 ggcagcggtctgcaacgcaaccccaacgctgctgcgcgtgcgcagcggtcttcgc 212  
63 GGCAGCGGCTTGGCAGCGCCCAACCAACGCTGCGCGCGCACCGCTTTCGCG 122  
273 ggcgcgctgcttctgctgtagcagcagcagcagcagcagcagcagcagcagcagc 332  
123 GCACGCTGCTTCTGCTTGGAGCAGCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 182  
333 gggcaccaccagcagcaacagcagcagcagcagcagcagcagcagcagcagcagcagc 392  
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363 CAGCACCAGGTAACAGGAGCTGAGAGTGAGCGCGCGCTCATGACATTGTGGCTTT 422  
573 ccagagacatcctcaagaagcagcagcagcagcagcagcagcagcagcagcagcagc 632  
423 CCAGGACATCTCATCAAGAGGCTGACGCGCTGCTGACGAGCCCTTCCAGCCCGGAGG 482  
633 ctggagctccagacacacagcagcagcagcagcagcagcagcagcagcagcagcagc 692  
483 CTGGGCTCCACACCAAGGCGGGCGCGCGCGCTTTCACATGAGCTGAGCTGGCGGCT 542  
693 caagagctcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 752  
543 CACGAGACTCTTGGGGCGCAGAGCAGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 601  
753 cgtggc 758  
602 CGTGGC 607

RESULT	2
LOCUS	BE878006
DEFINITION	BE878006 679 bp mRNA
ACCESSION	601849784F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891908 5', mRNA sequence.
VERSION	BE878006
KEYWORDS	EST.
SOURCE	human. Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 679)
REFERENCE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	

Plate: L1AM9677 row: h column: 21  
High quality sequence stop: 672.  
Location/Qualifiers

source	1. 679
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGF:3891908"	
/clone_id="NH.MGC.69"	
/tissue_type="large cell carcinoma, undifferentiated"	
/lab_host="DH10B (phage-resistant)"	
/note="Organ: lung; vector: pCMV.SPORT; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.1 Kb. Library constructed by Life Technologies."	
BASE COUNT	113 a 239 c 204 g 123 t
ORIGIN	

[illegible][illegible]

RESULT	3				
BF339551					
LOCUS		874 bp	mRNA		22-NOV-2000
DEFINITION	602033010F1	NCI_CGAP_Brn64	Homo sapiens	EST	IMAGE:4186995
ACCESSION	5', mRNA sequence.				
VERSION	BF339551				
KEYWORDS	BF339551.1	GI:11286006			
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (bases 1 to 874)		
	NIH-MGC	<a href="http://mhc.nci.nih.gov/">http://mhc.nci.nih.gov/</a> .		
	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: <a href="mailto:gsabss-remail.nih.gov">gsabss-remail.nih.gov</a>			
	Tissue Procurement: David N Louis, M.D.			
	CDNA Library Preparation: Life Technologies, Inc.			
	CDNA Library Arrayed by: Incyte Genomics, Inc.			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/ILNL at:			
	<a href="http://image.llnl.gov">http://image.llnl.gov</a>			
	Plate: ILAM9508	row: p	column: 04	
	High quality sequence stop: 701.			

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FEATURES
source
    Location/Qualifiers
      1..874
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:418695"
        /clone_lib="NCI-GCAP-Brn64"
        /tissue_type="glioblastoma with EGFR amplification"
        /lab_host="DHL0B (T1 phase-resistant)"
        /note="Organ: brain; Vector: PCMV-SpOrf6; Site: 1; Note:
      Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dt.
      Average insert size 1.57 kb. Constructed by Life
      Technologies. Note: this is a NCI-GCAP library."
BASE COUNT
129 a
299 c
301 g
145 t
ORIGIN
Query Match
Best Local Similarity 61.3%; Score 496.8; DB 147; Length 874;
Matches 565; Conservative 0; Mismatches 77; Indels 2; Gaps 2
OY 1 gcaagaaacacccactccctcgcgggagcgcagagacagggagcgcgtgtgtgcgc 60
Db 188 GCAGAAACACCCACTTCCCTCGCGGAGCAGAGAGACAGAGGAGGCGTGTGTGCACC 247
OY 61 cagtcgccccacagacatttgtgaagcggcgctgtgccgcagacagcccaagcgtgt 120
Db 248 CAGTGCCTCCCGAGGCACCTTTGTGCAGCGGGCGGTGCGCCGAGACAGCCCCACGCAGTGT 307
OY 121 ggcctcggttcacacgcgcacactacacgaagttcttggaactaaccttgagagcttcgcgcgtac 180

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```
Db 308 GGGCCGTCACACCGCCACTACACGACTTCTGGAACTACCTGGAGCGCTGCCGCTAC 367
181 tgaacatctcttgcgagagagcgttgaagagagagcagagcgttgcacagccacacac 240
368 TGCAGACTCTCTGCGGGGAGCGGTGAGAGAGAGCAGGGCTTCCACGACCCACACAC 427
Qy 241 cgtgctgcgcgtgcgcagcgcgttcttcgcgcagcgtggttcttgcgttgcagcga 300
428 CGTGCTGCGCGCTGCCACCGCGCTTCTTGCGCGCACCTGCTTCTGAGTGGAGCAGCA 487
Qy 301 tctgtaccactgtgtgcgcgcgttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 360
488 TCGGTCCACCTGCTGCGCGGTGATGCCCCGGGCAACCCACCCAGAACACCACTGTC 547
Db 361 caagcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 420
548 CAGGTCGCCCCCGACGCAACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCACTGCCACCC 607
Qy 421 caacgcaactgcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 480
608 CACCG-AACTGCAAGCGCTGGGCGCTGCCCTCAATGTGCGAGGCTCTCTCCATGAC 666
Qy 481 accctgtgcacacgcgtgcacgtgttccctccacgcgcgcgcgcgcgcgcgcgcgcgcgc 540
667 ACCCTGTGCAACGACGTCGACTGGTTCCTCCCTCAGCA-CAGGGTACAGAGGTTGATGAG 725
Db 541 tgtgaagtgctgcgtgcacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
726 TGTGAGCGTCCCTGCTTCTGAGTTGTGCTTCCAGGAGGACTTCTCATTCAAGAGGTGCCGC 785
Qy 601 cgcgtgtgcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 644
786 GTGTGGGCTTGAAGCCGAGAGGTGGGTGCGCGCAGGGGGGCGGC 829
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RESULT 4
LOCUS AW083241/c
DEFINITION x07604.x1 NCI-CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583534.3'
similar to TR:095407 095407 DECOY RECEPTOR 3.; contains 11 bp MER22
repetitive element;; mRNA sequence.
ACCESSION AW083241
VERSION AW083241.1 GI:6038393
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 692)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bdnp/image/image.html
Seq primer: -40UP from Glibco
High quality sequence stop: 414.
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## FEATURES

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1..692
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2583534"
/clone_1b="NCI-CGAP_Co21"
/tissue_type="moderately differentiated adenocarcinoma"
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```
/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Normalized to cot >500. Average insert size 1.04kb.
Library constructed by Life Technologies."
```

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BASE COUNT 136 a 205 c 235 g 115 t 1 others
ORIGIN
Query Match 59.6%; Score 482.6; DB 111; Length 692;
Best Local Similarity 97.7%; Pred. No. 9; Se-89;
Matches 510; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
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Qy 290 tgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 349
619 TGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 561
Db 619 TGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 561
Qy 350 acacgagtgccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 409
560 ACACGAGTGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 501
Db 560 ACACGAGTGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 501
Qy 410 agtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 469
500 AGTGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 441
Db 500 AGTGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 441
Qy 470 cctccatgaacacctgtgcacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 529
440 CTTCCTCATGACACCTGTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 381
Db 440 CTTCCTCATGACACCTGTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 381
Qy 530 gagctgaagagtgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 589
380 GAGCTGAGAGATGTGAGCAGTCCGTCATGACCTTGTGAGCTTCCAGAGCATCTCATATCA 321
Db 380 GAGCTGAGAGATGTGAGCAGTCCGTCATGACCTTGTGAGCTTCCAGAGCATCTCATATCA 321
Qy 590 agagagctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 649
320 AGAGGCTGCAAGCGGCTGCTGAGGCGCTCGAGGCGCCGAGAGGCGTGGGGTCCGACACAA 261
Db 320 AGAGGCTGCAAGCGGCTGCTGAGGCGCTCGAGGCGCCGAGAGGCGTGGGGTCCGACACAA 261
Qy 650 ggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 708
260 GGGCGGCGCGCGCGCGCTTGCAGCTGAACCTGCGTGGCGCGCTCACAGGAGCTCTTGGGG 201
Db 260 GGGCGGCGCGCGCGCGCTTGCAGCTGAACCTGCGTGGCGCGCTCACAGGAGCTCTTGGGG 201
Qy 709 gcgcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 768
200 GCGCAGAGCAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 141
Db 200 GCGCAGAGCAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 141
Qy 769 ggcgtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 810
140 GGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 99
Db 140 GGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 99
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```
RESULT 5
LOCUS AW262121/c
DEFINITION xq31004.x1 NCI-CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752231.3'
similar to TR:095407 095407 DECOY RECEPTOR 3.; contains 741 bp
TARI repetitive element;; mRNA sequence.
ACCESSION AW262121
VERSION AW262121.1 GI:6638937
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 600)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
```









COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL, send email to: info@image.lnl.gov  
Seq primer: -400P from Gibco  
High quality sequence stop: 419.

FEATURES  
source  
1. 478  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1ib="NCI-CGAP-Co16"  
/tissue\_type="colon tumor, RER"  
/lab\_host="DH10B"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: NotI; Site\_2: EcoRI; Plasmid DNA from the normalized library NCI-CGAP-Co10 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1057416-1061255, and 114584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT  
108 a 146 c 144 g 80 t  
ORIGIN

Query Match 44.3%; Score 359; DB 143; Length 478;  
Best Local Similarity 100.0%; Pred. No. 1.4e-63;  
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 452 tcaatgctccagagctctctccatgacacccctgtgacccagctgacgtctccccc 511  
Db 478 TCAATGCTCCAGAGCTTCTCTCCATGACACCCCTGTGACCGCTGGCTGCC 419

QY 512 tcaagaccagaggtacccagagctgagagctgagcgtgacgtatcagacttggctt 511  
Db 512 TCAAGACCAGAGGTACCCAGAGCTGAGAGCTGAGCGTGCCTGATCAGACTTGTGCTT 359

QY 418 TCAGCACCAGGATGACGAGAGCTGAGAGCTGAGCGTGCCTGATCAGACTTGTGCTT 359  
Db 418 TCAGCACCAGGATGACGAGAGCTGAGAGCTGAGCGTGCCTGATCAGACTTGTGCTT 359

QY 572 tcagagacatcgtatgaagagctgacagctgctcagagcctcagagcccgagag 631  
Db 572 TCAGAGACATCTCATTGAAGAGCTGACAGCGCTGCTCAGAGCCCTCAGAGCCCGAGG 299

QY 632 gctggggtcgcagacaaaggcgagcgctgtcagctgaaagctgcgtcgcgcgc 691  
Db 632 GCTGGGgtcgcagacaaaggcgagcgctgtcagctgaaagctgcgtcgcgcgc 691

QY 298 gctgggggtcgcagacaaaggcgagcgctgtcagctgaaagctgcgtcgcgcgc 239  
Db 298 GCTGGGGgtcgcagacaaaggcgagcgctgtcagctgaaagctgcgtcgcgcgc 239

QY 692 tcaagagactcctggggcgagagcgctgctgctgctgctgctgctgctgctgctg 751  
Db 692 TCAAGAGACTCTCTGGGGCGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 179

QY 752 gctggggtcgcagacaaaggcgagcgctgtcagctgaaagctgcgtcgcgcgc 810  
Db 752 GCTGGGgtcgcagacaaaggcgagcgctgtcagctgaaagctgcgtcgcgcgc 810

Db 178 GCTGGGgtcgcagacaaaggcgagcgctgtcagctgaaagctgcgtcgcgcgc 120

RESULT 13  
LOCUS AM083914 515 bp mRNA EST 14-OCT-1999  
DEFINITION xc25902.x1 NCI-CGAP.Co19 Homo sapiens cDNA clone IMAGE:2585330 3'  
similar to TR:095407 095407 DECOY RECEPTOR 3. ;, mRNA sequence.  
ACCESSION AM083914  
VERSION AM083914.1 GI:6039066  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 515)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL, at: www.bio.lnl.gov/bdrp/image/image.html  
Seq primer: -400P from Gibco  
High quality sequence stop: 355.

FEATURES  
source  
1. 515  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1ib="NCI-CGAP-Co19"  
/tissue\_type="moderately differentiated adenocarcinoma"  
/lab\_host="DH10B"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Normalized to Cot 50. Average insert size 1.32kb. Normalized version of NCI-CGAP-Co18. Library constructed by Life Technologies."

BASE COUNT  
102 a 160 c 158 g 94 t 1 others  
ORIGIN

Query Match 43.7%; Score 354; DB 111; Length 515;  
Best Local Similarity 94.4%; Pred. No. 1.5e-62;  
Matches 388; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

QY 400 agctcaagagcagtgccagcccccagaaactgaagcagcctgagcctgacctaagt 459  
Db 400 AGCTCAAGAGCAGTGCCAGCCCCCAGAAACTGAAGCAGCCTGAGCCTGACCTAAGTG 456

QY 515 AGCTCAGAGCAGTGACACCCCGCAAAATGCGGCGCTTGGCTGAGCCCTTAAGTG 456  
Db 515 AGCTCAGAGCAGTGACACCCCGCAAAATGCGGCGCTTGGCTGAGCCCTTAAGTG 456

QY 460 ccaagctctctccatgaagacccctgtagcagcagctgcttccctcagcacc 519  
Db 460 CCAAGCTCTCTCCATGAAGACCCCTGTAGCAGCAGCTGCTTCCCTCAGCACC 396

QY 455 CCAAGCTCTCTCCATGAAGACCCCTGTAGCAGCAGCTGCTTCCCTCAGCACC 396  
Db 455 CCAAGCTCTCTCCATGAAGACCCCTGTAGCAGCAGCTGCTTCCCTCAGCACC 396

QY 520 aaggttaccagagctgagagtgtagcgtgacgtatcagacttggcttccagagac 579  
Db 520 AAGGTTACCAGAGCTGAGAGTGTAGCGTGTAGCGCTGATCGACTTGTGCTTCCAGAGAC 336

QY 395 AGGTTACCAAGAGCTGAGAGTGAGCGTGTAGCGCTGATCGACTTGTGCTTCCAGAGAC 336  
Db 395 AGGTTACCAAGAGCTGAGAGTGAGCGTGTAGCGCTGATCGACTTGTGCTTCCAGAGAC 336

QY 580 attccatcaagagctgtagcagcgtgctgtagcagcctcagagcccgagagctggagt 639  
Db 580 ATTCCATCAAGAGCTGTAGCAGCGTGTGAGCGCTGTGAGCGCTTCCAGAGCGCTGGAGT 277

QY 335 ATTCCATCAAGAGCTGAGAGTGAGCGTGTGAGCGCTTCCAGAGCGCTGGAGT 277  
Db 335 ATTCCATCAAGAGCTGAGAGTGAGCGTGTGAGCGCTTCCAGAGCGCTGGAGT 277

QY 640 ccgaacacaaaggcgagcgcgctgtagcagctgtagcagctgtagcagctgtagcag 699  
Db 640 CCGAACACAAAGGCGAGCGCGCTGTAGCAGCTGTAGCAGCTGTAGCAGCTGTAGCAG 218

QY 700 ctccctggagggcgagagcgagcgctgtagcagctgtagcagctgtagcagctgtagc 759  
Db 700 CTCCCTGGAGGGCGAGAGCGAGCGCGCTGTAGCAGCTGTAGCAGCTGTAGCAGCTGTAGC 158

QY 217 CTCTGTGGGGGCGAGAGCGGCGCGCTGTAGCAGCTGTAGCAGCTGTAGCAGCTGTAGC 158  
Db 217 CTCTGTGGGGGCGAGAGCGGCGCGCTGTAGCAGCTGTAGCAGCTGTAGCAGCTGTAGC 158

QY 760 aggatgcgcggagctgtagcagcgtcctgtagcagcttccctcctgtagcag 810  
Db 760 AGGATGCgcggagctgtagcagcgtcctgtagcagcttccctcctgtagcag 107

RESULT 14  
LOCUS AM014771 459 bp mRNA EST 10-SEP-1999  
DEFINITION UT-H-B10-aag-g-04-0-UT.si NCI-CGAP-Sub1 Homo sapiens cDNA clone IMAGE:2709294 3', mRNA sequence.

ACCESSION AW014771 GI:5863528  
VERSION AW014771.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 459)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA library preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
www.bio.lnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward  
POLA=yes

## FEATURES

source

Location/Qualifiers  
1..459  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2709294"  
/clone\_1lb="NCI-CGAP\_Sub1"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; The  
NCI-CGAP Sub1 library is a subtracted library derived from  
B1. B1 constitutes a mixture of 21 normalized or  
subtracted NCI-CGAP libraries: NCI-CGAP\_C04,  
NCI-CGAP\_Pr22, NCI-CGAP\_Pr28, NCI-CGAP\_C010, NCI-CGAP\_C016,  
NCI-CGAP\_Kid5, NCI-CGAP\_Kid12, NCI-CGAP\_Kid3,  
NCI-CGAP\_Kid11, NCI-CGAP\_Lym2, NCI-CGAP\_Pr23, NCI-CGAP\_C08,  
NCI-CGAP\_C011, NCI-CGAP\_Le12, NCI-CGAP\_Brn23, NCI-CGAP\_Lu5,  
NCI-CGAP\_Lu24, NCI-CGAP\_Lu19, NCI-CGAP\_GC4, NCI-CGAP\_GC6,  
NCI-CGAP\_Brn25. These 21 libraries were pooled and a  
single-stranded DNA preparation of the resulting mixture  
was used as a tracer in a subtractive hybridization with a  
driver whose composition is detailed below: NCI-CGAP\_Kid3  
pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE  
CloneIDs 1322376-1323911, 1456008-1456775, 1500522-1502855  
); NCI-CGAP\_Kid5 pool 1 LLAM 3338-3342, 3722-3725,  
3776-3778 (IMAGE CloneIDs 132912-132831,  
147168-1472903, 1492104-1493253); NCI-CGAP\_Lu5 pool 1 LLAM  
3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,  
1520904-1522439); NCI-CGAP\_GC4 pool 1 LLAM 3164-3167,  
3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,  
1469064-1470983, 1475592-1476743); NCI-CGAP\_Pr22 pool 1  
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs  
985608-986759, 1101192-1101959, 1217928-1220615)  
NCI-CGAP\_C010 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE  
CloneIDs 1057416-1061255, 1144584-1145351) The resulting  
subtracted library contained 530,000 recombinants.  
Subtraction was performed as previously described [Bonaldi  
& Soares (1996): Normalization and Subtraction:  
Two Approaches To Facilitate Gene Discovery. Genome  
Research 6, 791-806.  
TAG\_LIB=NCI-CGAP\_C04  
TAG\_TISSUE=COLON  
TAG\_SEQ=CTTGC

BASE COUNT 93 a 143 c 136 g 87 t  
ORIGIN

Query Match 42.6%; Score 345.2; DB 110; Length 459;  
Best local Similarity 99.1%; Pred No. 9.4e-61;  
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Db 459 CAGGCTCTTCTCTCCATGACACCCCTGTGCACAGCTGCACTGGCTTCCCTCAGACCA 400  
QY 521 ggttaccagagctgaggtgtgagcgtgctcgtatcagacttctggtcttcaggaca 580  
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Db 399 GGGTACCAGAGGTGAGGATGTGAGGTGTCCTCATGACTTGTGGCTTCCAGACCA 340  
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Db 339 TCTCCATCAAGAGGCTGACAGCGGTCTCTGACAGCCCTCGAGGCCCGGAGGCTGGGGTC 280  
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QY 761 ggttcgccgagctgagcgagcgagcgtccgtagcgcttcctcctgtgacac 810  
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RESULT 15  
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 445)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.lnl.gov/bbrp/image/image.html  
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## FEATURES

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Best Local Similarity 100.0%; Pred. No. 2e-56;  
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